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Copyright (c) 1993 - 2000 Compugen Ltd.
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ORGANISM JOURNAL MEDLINE REFERENCE AUTHORS RESULT 1
AF041051
LOCUS
DEFINITION REFERENCE AUTHORS TITLE Compartmentalized expression of two structurally and functionally distinct 4-coumarate:CoA ligase genes in aspen (Populus tremuloides) Hu, W.J., Kawaoka, A., Chiang, V.L. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I Malpighiales; Salicaceae; Populus.

1 (bases 1 to 1172) AF041051 1172 bp DNA linear PLN 26-JUN-1998 Populus tremuloides clone Pt4CLlp 4-coumarate:CoA ligase gene, promoter region.
AF041051 AF041051.1 GI:3258638 2 (bases 1 to 1172)
Hu, W.-J. and Chiang, V.L. Proc. Natl. 98226828 Populus tremuloides quaking aspen. Acad. Sci. U.S.A. Tsai, C.J., Lung, J., Osakabe, K., Ebinuma, H. and 95 (9), 5407-5412 (1998) 4

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Lu,H., Zeng,Q. and Jiang,X.
Direct Submission
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Qinghua East Road No. 35,
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RVFFIEAIPKAPSGKILKKNIKEKAGI"
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                     aaggttaatagaggtagttgtgattgagatatgtccagcactagtttttttgttggtgtga
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On Apr 2, 1999 this sequence version replaced gi:4337172.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hyman,R.W., Fung,E.L., Qin,F., and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCUUDDU4 104992 bp DNA linear Plasmodium falciparum chromosome 12, *** SEQUENCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (21-AUG-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hyman, R.W., Qin, F., Fung, E.L., Conway, A.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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                                                         Similarity 45.3
02; Conservative
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                                                                                                                                                                                                                                                                                                            as soon as it is available and the accession number be preserved.
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/db_xref="taxon:5833"
/chromosome="12"
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Stanford University, 855
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58842: gap of unknown length
91011: contig of 32169 bp in
91211: gap of unknown length
104992: contig of 13781 bp in
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                                                           Score 83; DB 2;
Pred. No. 6.8e-05;
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On Aug
* NOTE
                                                                                                                                                                                                                                                                                                                                                                    AC004157 169546 bp Plasmodium falciparum chromosome PROGRESS ***, 2 unordered pieces.
                                                                                                                 Direct Submission
Submitted (19-FEB-1998) Stanford DNA Sequencing and Technology
Center, Stanford University, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                             HTG;
                                                                                                                                                                 2 (bases 1 to 169546)
Hyman, R.W., Qin, F., Fung, E.L.,
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AC004157.8 GI:9797712
                                                                                                                                                                                                  Unpublished
arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
                                         n Aug 12, 2000 this sequence version replaced gi:8810447 NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                             HTGS_PHASE1.
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3D7, ***
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AL133402/c LOCUS DEFINITION

AL133402 Human DNA :

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93368 bp DNA 1: clone RP5-1077H22 on

linear

chromosome

24-JUL-2000 6. Contains

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                                                                                                                                        AAAAAAATATAATTAAATTAATTAATTAATTAAATATATTTAATAGTAATTAAATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ttctaataaagcacttcctaattgttaaaatatatgtctaaacactaataataaaattta 732
                                                                                                                                                    atggatt
                                            TTATAATTATATATATATTAATAATTAATTTAAAATATAAATTAAGAAAGATAATTTT
                                                         tttgtgtatctttggcagtaggtgagaggtgctgacaaataaaattagtgcataaaatata
                                                                                          taaatgattaacctttaaatctcgagtttctcttataaaaaacacgtataattgggctag
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Similarity 45.38;
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85625
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/db_xref="taxon:5833"
/chromosome="12"
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15381 c 1
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23666: gap of unknown length
169546: contig of 145880 bp in lengt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15705 g
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Pred. No. 6.1e-05;
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REFERENCE
AUTHORS
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ORGANISM
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KEYWORDS
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AL133402
AL133402.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   on May 23, 2000 this sequence version replaced gi:7939106. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; i
Mammalia; Eu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/HGP/Chr6
RP5-1077H22 is from the library RPCI-5 constructed at the Park Cancer Institute by the group of Pieter de Jong. For details see http://bacpac.med.buffalo.edu/
VECTOR: pCYPAC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw:, SWISSPOT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (18-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 23, 2000 this sequence version replaced gi:7939106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          feature key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    putative novel gene,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence is the entire insert of clone RP5-1077H22
                                      /note="match: GSS: Em:AQ984702"
9599. .9750
                                                                           /note="LIPB2 repeat: 9565..9598
                                                                                                             /note="L1PBa repeat:
7856. .9561
                                                                                                                                                                                              6632.
                                                                                                                                                                                                                                     /note="L1PBa repeat: matches -1546.
4721. .6631
                                                                                                                                                                                                                                                                           4299
                                                                                                                                                                                                                                                                                                                /note="AluSq repeat: matches 1.
complement(3971. .4298)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="RPCI-5"
231. .537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
/chromosome="6"
/clone="RP5-1077H22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Eutheria; Primates;
                                                                                                                                                                    5632. .6939
/note="Alu<u>Y</u> repeat: matches 3.
                                                                                                                                                                                                                                                                                            'note="match: GSS: Em:AQ720689"
                                                                                                                                                                                                                                                                                                                                                                         'note="MIR repeat: matches 30.
                                                                                                                                                                                                                                                                                                                                                                                                             note="AluSx repeat: matches 39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="AluY repeat: matches 1. .301 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism≂"Homo sapiens"
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  "4 copies 38
.9739
                                                                                                                                                                                                                 LlPBa repeat: matches -134.
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                                                                                                                                     matches 2762.
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                                                                                                 matches
                      71% conserved"
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                                                                                                                                                                                                                                                                                                                                    .304 of consensus
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                                                                                                                                   .3638 of consensus
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                                                                                                                                                                                                                                                     .-1136 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                     /note="Alux
14897. .1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="AluJo repeat: matches 1.
11341. .11501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9806. .9841
/note="match: GSS: Em:AG026544"
9807. .9841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9803.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="match: 9797. .9841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="match: GSS: 9797. .9824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="match: GSS: 9797. .9828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="match: GSS: Em:AQ745266" 9796. .9824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="match: 9796. .9823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="match: GSS: 9796...9835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="match: GSS: Em:AZ110479" complement(9796. .9835)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="match: GSS:
complement(9764. .
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9708. 9831
                                                                                                                                                                                                                                                     complement (19549)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MLT1B repeat: matches 1. 13221. .13307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(9796
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                                                                                                                                                                                                             /note="match: GSS: Em:AQ734906"
join(<21618. .21754,25301. .>25
                                                                                                                                                                                                                                                                                                                                  /note="L1PB2 repeat: matches 5782. .6154 of consensus"
10724. .11003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9708. .9831
/note="match: STS:
                                                                                                                 /product="dJ1077H22.1 (putative novel protein)"
join(21618. .21754,25301. .25566)
                                                                                                                                                                                                                                                                                                /note="MER66B repeat: matches 1.
17062. .17326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="match: GSS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="match: GSS: Em:AQ014122
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  /note="MIR repeat: matches 43.
26551. .26628
                                                          note="MER33
                                                                                               join(21618. .21754,
/gene="dJ1077H22.1"
                                                                                                                                                        /evidence=not_experimental
                                                                                                                                                                      note="match: ESTs: Em:AA960797"
                                                                                                                                                                                              /gene="dJ1077H22.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MER5B repeat: matches 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="match: GSS: Em:AZ028723"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="match: GSS: Em:AQ598220"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .9824
                                    "MER33 repeat: matches 7. .323 of consensus" .25647
                                                                                                                                                                                                                                                                                                                                                                                                                                                      .13693
                                                                                                                                                                                                                                                                                                                                                                           .15051
                                                                                                                                                                                                                                                                                                                                                                                                           ALl repeat: matches 595. .1036 of consensus"
14463
                                                                                                                                                                                                                                                                                                                                                                                         repeat: matches 1. .296 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat: matches 550.
                                                                                                                                                                                                                                                                       repeat: matches 28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Em: AQ014122"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Em: AQ598220"
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                    .246 of consensus"
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/note==33 copies 4 mer 9
46483. 46558
/note==38 copies 2 mer 9
47326. 47676
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/note="28 copies 4 mer tata 67% conserved"
38001. .38112
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/note="L2 repeat: matches 2677. .2710 of consensus"

34405. 34634

/note="LIMB8 repeat: matches 5857. .6120 of consensus"
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41413. .41819
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27163. .27450
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                                                                                                                                                                                                                                                                                                                                                                                                 /note="4 copies 39
46452. .46565
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46228. .46383
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46186. .46375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MIR repeat: matches 21. .146 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="match: GSS: Em:AQ430150
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43137. .43480
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42349. .42490
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41820. .41874
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37654. .37931
note="LLMC5 repeat: matches 7507. .7777 of consens
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37369. .37635
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47.78;
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---GTATATAATATATATATATATAAAATATATA 77569
                                                                                                                                                                                                                                            Score 82.2; DB 9;
Pred. No. 9.5e-05;
0; Mismatches 298;
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                                                                                                                                                                                                                                                                                        Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 20, 2001 this sequence version replaced gi:15148276. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boushayki, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
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Birren, B., Linton, L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                     http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                 Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                             Center code: WIBR
                                                                                                                                                                                    Center: Whitehead Institute/ MIT Center
                                                                                                                                                                                                                          -- Genome Center
                                      Project
name: L5662
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SEQUENCING
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hes 224; Conserv
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1 155157: contig of 155157 bp in length
155158 155257: gap of 100 bp
155258 185699: contig of 30442 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
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Pred. No. 0.00012;
0; Mismatches 338;
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VOO3 60 amino acid repeat gene fami	
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Location/Qualifiers 1. 236120	FEATURES source
Submitted (00-MAI-1998) MICRODIOLOGY, Film Island Animal Disease Center, U.S. Dept. Agriculture, Agricultural Research Service, P. Box 848, Greenport, NY 11944-0848, USA	CORNAL
1000 Minsprinter of the Table 3 tens of the table of table o	TITLE
1 to 236120)	REFERENCE
Afonso, C.L., Tulman, E.R., Lu, Z., Oma, E., Kutish, G.F. and Rock, D.L. The genome of Melanoplus sanguinipes entomopoxvirus J. Virol. 73 (1), 533-552 (1999)	AUTHORS TITLE JOURNAL
u u	SOURCE
AF063866.1 GI:4049647	ACCESSION VERSION KEYWORDS
AF063866 236120 bp DNA linear VRL 22-DEC-1998 Melanoplus sanguinipes entomopoxvirus, complete genome.	LOCUS

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CDS
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CTAATTCTTTCAAATTATCTAAATTAATTATAAAATTAGTATTTTTTATATTACATGAAC
                                                                                                                                                                                                                                                                                                                                                  aggtgaccagttgtcaaatgaccactcgacttggggcatggtgattttttcaaatcacaac 352
                                                                                                                                                                                       gaataatatgattgattattctctgtaattttgtgaaatagattaaaacagctcaatgtg 292
                                                                                ATATATCCAATTCTTTTAAATTAATTAAATTTAAAGAACTAGCATTTATTATATTAC
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NNIISNISNYKLSKTIKKFICARCAITDFTFLEELINLEILDVSYNHKLNISECELPI
SLKKLYCNNCFIKNNTLLKKLINLTILNISFNKITDFKFLENLTNLEILDISENKNSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYFSHYKSKYIKILNCEKCNIKDFKFLEKLSNLEILNISDNKNSNISKCNLPNKIKKF
ICVRCDIKDFWFLEKLFRLOMLDISYMYIKSNISKCKLPISLIELYCKNCTNNWFYFL
NDLPRLEILDISCNNKIININNIRLSKKLIKLNCSNNNISDIKFLEHLSKLNLEILNISY
NKISYIYNYKLPNNLEELNCKYNNIKWFFIERLHNLKKLNISNNKKSNISKCKLPQT
IINLAIKACDITDESFLEPLANLEKLMITEENYDNETMLSKCKLPVSLRVLKSTDFNV
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CSDCYKTKDFKFLERLINLQKLNISYTFSSNISTCELTSTLVELNCSTCKINNFTFIE
KLYNLKILDINNNPNSNISECKLSTALIELDCTICNITDFKFLEPLINLQKLNICGNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="ORF MSV013 leucine rich repeat gene family protein, similar to Amsacta moorei entomopoxvirus Q3 SW:P28854"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="muninlycyeisnickffsfskniklvileilhlnsinlfgnlh
SDIFEFSLQNIFNIFRLHKDSKNLKSIISLIIQSNSINDIGNLQLDIFEFLLYDIINF
FKLCNFSKNVKSIIIQDEQSNILIDEGI"
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/codon_start=1
/codon_start=1
/product="ORF MSV012 hypothetical protein"
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/protein_id="AAC97651"
/db_xref="G1:4049651"
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KKLNISDNRNLKITECKLPISLIELDCSSCDITDFKFLEPLINLKKLNISDSRNLKII
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/db_xref="GI:4049650"
/translation="MNNINLYCYENLLKYLDDKNKHKLAKVSKIFQYYNYQLNIDIHY
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/translation="MNINIXCYENLIKYLKDSDIHNLASICELFQYYNYOLNICVNH
/translation="MNINIXCYENLIKYLKDSDIHNLASICELFQYYNYOLNICVNKI
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/gene="MSV013"
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/gene="MSV013"
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15855. .16247
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/codon_start=1
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On Dec 16, 19
For more info
                                                                                                                                                                                                                                                                                                                                     correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
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AL031746.9 GI:6594243
                                                                                                                                                                                                                                                                                                                    phage etc
                                                                                                                                                                                                                                                                                                                                                                                                                 see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORTANT: sequence is unfinished and does not necessarily represent the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (24-SEP-1998) P.falciparum Genome Sequencing The Sanger Centre, Wellcome Trust Genome Campus, Hinxto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barrell, B.
    overlap)"
                                                       aa, similarity: UPF0006 family
YBL055C/YBL0512/YBL0511, YBF5_1
                                                                                                               complement(join(1748. .2598,2748. .2848,2990. /gene="MALIP3.01"
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/gene="MAL1P3.01"
                                                                                           /note="MAL1P3.01, conserved hypothetical
                                                                                                                                                                                                                                     /organism="Plasmodium
/strain="3D7"
/codon_start=1
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BL0511, YBF5_YEAST (418 aa), fasta
E(): 1.1e-12, (33.2% identity in 271
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                                                                               NHLQNDAPYNTYKKFSQTEIDEISRDFLSIGKNASSSSGIKNNIKNIIDNIKFYEN
DYIINBIKSTKKMEKOSLNENRSLPNVNIYN KMESOVBSYTFFYTJSCIRLFNVFVKIF
MSFYVFHIKIGSNSVGIAIMLSILALYSAMILFEELSSLFKSKYLLIYRDKRIDNMHIVL
KEFKLIKMFNMESFAFKYINIFRMKEKKYCKIRLYLSNIGUFISSISDIVEVUIFFI
YLKDRLNKKEEIKFTSIIMPLYVYKILISNVANFPNLVNNVMEGIVNIKRLNNYINDH
LYYNDIKNYFMYRTRYNBDYNIVODKTFLQNENITSHDOGTSHNLKHLKNVIKNLINN
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KKEEYENIHNSSNSTMSNEFKEKKKNNEYIIKLENCSFGLSYDNKCDNDHILKNINN
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KKEEYENIHNSSNSTMSNEFKEKKKNNEYIIKLENCSFGLSYDNKCDNDHILKNINPN
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NIRSMILFGNEYNFLIYKYTILQSELLNDLSTIEHGDMKYINDHNLSKGOKVRICLA
RALYEHYIHMHKLCTOYEKKLIQDPNEILDKDLINNKNISSYNNKKSKLVWYNIFPNEN
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TLDNFRIKFDEVELNYKHSMKNIYKRDAFVKCNTESVSFEIDSINKEYIKKMKKNY
KKEHMNKNNKDNNNNNNNKDDHININNNDNHRNYNDINLGPNSTDDSPTVSSLGNE
YTLDTTRKKFENYKWENT
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complement(2742 ..2747)
/gene="MALLP3.01"
YNNNLGNIINRFIIDISAFDYGFLKRIYKAFFIFFRCILSSLLIIYMIRDCIFIFPFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YISFLKDFKVFSGLVVVMIMFFHLFFEALLHFYFHLFTINLKVSLMYFLYKINLCSNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MTTYKENVGISNKGNKKKKSCQNISFLNFLSFDWIRPLINDLIK
GDIQELPNICRNFDVPYYASKLEENLRDIEVEDSEFYSEKNSSNEHVLHHCNSNDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="putative ABC transporter"
/protein_id="CAB63558.1"
/db_xref="GI:6594246"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"hypothetical protein, MAL1P3.02"
/protein_id="CAB63557.1"
/db_xref="G1:6594245"
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AMRKLLSGEINSIKLDNGDELKIKLNDEKHKDSTKWDKSYSFISNLEEEKYSQTDLFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contains possible signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(2984. .2989)
/gene="MAL1P3.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="potential splice complement(2849. .2861) /gene="MALLP3.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="MAL1P3.01"
/note=""""
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSLKSLENINAVKKIPLNLLLLETDAPWCGVKKTHASYEYIKDTYEKRAYTNLKKIKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEKDKEYLENLKNKIIKYPNRIYCIGEIGLDFDRLYFCSKYIQIKYFIFQLKLYQMFN
LPMFLHMRNCSETFFKIYDIYKFLFEKNGGYIHSFTDKEDIVHIIVQNYKNLYIGVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNNVDKIIITCTCLAEIDKSLKICETYDPEGKFLYLSAGVHPTNCYEFIDKNKHEEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MKLVFHYIKYINVLFYISIIFLKSNSLKIYNDLRYISTVNKYKV
LQIKKRSNLKKNHNIRKMEDNESSFIDIGSNLTDKMFDGVYNSKKHENDLQNVLNRAK
                                                              FKGSISLETYLWYFQQVGFVLLTSVVIFMLISIFTDEIKFVFLTMMSIISKNNKEHSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="MAL1P3.03"
/note="MAL1P3.03,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="MAL1P3.03"
14884. .20352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14884.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKQEINEANTKIIEDRQEFYILNNDEIENIATRFVLENNFDELYIQSFKQSLIDIIQS
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/db_xref="GI:6594244"
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/protein_id="CAB63556.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="possible cen1,
14884. .20352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MAL1P3.02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="potential splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="MAL1P3.02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note='
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="MAL1P3.02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .5496
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                 /gene="garp"
complement(join(38049. .39995,40210.
                                                                                                                                                                                                                                                                                                                                                                                         /gene="MALIP3.05"
/note="potential splice
complement(join(38049.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="potential splice donor sequence,
36854. .36863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mrikmusgiffikllicisficvfecfukcmisyrkdilmysen
Cfnysidrslaegssesketkvkdipniellkslninyeeyekmkeivgsfmdnunln
Ianevlknihsftnienifslindsskspvlktflkefgsifphmlnnvpkllfdlcq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(32669. .32674)
/gene="MALIP3.04"
/note="potential splice donor sequence,
join(3657. .36743,36864. .37343)
join(3657. .36743,36864. .37343)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HDKEETITTWIKWIQEDIEYFLFNLQVEWLRILTLELFYKNKE" complement(32477. .32486)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MKKSYTFINVTILLFLTLLLFLTYYNYDTFSKTKFNNNIKIDIN
RFKRIIAEASEEQKYPWEEDFCLILNEEELIRPEHNDSPYLPEHYENIDKINELSINS
TKIWKETIKKMRQNYEKETDNMNHNWRDFMWHYKWANIYLYKVHKLINITLKDLTNPI
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in 1
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/gene="MAL1P3.04"
/note="MAL1P3.04, conserved hypothetical membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(31966.
/gene="MAL1P3.04"
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23896. .31533
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KKIPLVNGTYKXIDEEPSLKNINMYALKNQKIGIVGKSGAKKSTILLSILGLINISQG
KITPLVNGTYKXIDEEPSLKNINMYALKNQKIGIVGKSGAKKSTILLSILGLINISQG
KITPLGENDIRTYNIKGEDSIIGILAQGSFVFVNWNIRTFIDPYNNFTDDEIVHALKLN
GINLGKNDLYKYMHKQDMKSNYKKIIQTSKVINQSNDNTILLTNDCIRTLSLYBLYLN
GINLGKNDLYKYMHKQDMKSNYKKIIQTSKVINQSNDNTILLTNDCIRTLSLYBLYLN
KITLIDEIPIFNLNNSYHDELNSFLIGKAKSFNYIIRNHFPNNTVLIISHHANT
KIEKKKKKQEEKEKKKQEKERKKQEKKERKQKEKEMKKQKKIEKERKKKEEKEKKKKK
                                                                                                                                                                                                                                                               /gene="garp"
/note="MALLP3.06, garp, len: 673 a
identical to GARP_PLAFF (678 aa),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36744. .36749
/gene="MAL1P3.05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="hypothetical protein, MAL1P3.05"
/protein id="cAB63560.1"
/db_xref="GI:6594248"
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/gene="MALIP3.04"
/note="potential splice acceptor sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="CAB63559.1"
/db_xref="GI:6594247"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="region containing small subunit,
subunit rRNA genes and spacer regions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23896. .31533
/gene="rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSCCDYIYVLRKGEITYRCSYEDVKTQSELSHLLEMDD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSTLGYCISFSARLGVIIKFLLCDYTHIEKEMCCVQRLEEFAKISNKENASMNKENEL
                                                                                                                                                                                                                                             identity in 678 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="MAL1P3.05"
/note="MAL1P3.05,
                                                                                                                                                                                                                        /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="conserved hypothetical membrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            n: 203 aa, similarity: P. falciparum chromosome 2, 80110W, 096126 predicted integral membrane protein (255), fasta scores: opt: 335, E(): 4.9e-15, (36.1% identity 191 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein,
                                                                                                                                                                                                                                                                                                                                                                                            .39995,40210. .4028
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                                                                                                                                                                                                                                                                                             673 aa, similarity:
                                                                                                                                                                                                                                                                      fasta scores:
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RESULT 9 AL513330/c

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Homo sapiens chromosome PROGRESS ***, 7 unordere

202645 bp DNA cromosome 1 clone RP11-469E8, unordered pieces.

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SEQUENCING

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acaattattaaaattaattattattttttctaataaagcacttcctaattgttaaaa 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAATAAATTAAATAAATAAATAA ---TAAAAATAATATATTAAAATATATAAAATTAACA 8143
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                                                                      tcttataaaaaacacgtataattgggctagatttaacagctattattcaaactggccagg 642
                                                                                                                                                                                                                        taatatcttatgtgatataatttagaaatataaatgattaacctttaaatctcgagtttc
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                                                                                                                                                                                                                                                                                                                                                                            attcacgggttggctaatcaattattattaattaaaaacgatagtatttttgataatttaa 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                    gtgaggtgaccagttgtcaaatgaccactcgacttggggcatggtgatttttcaaatcac 349
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EHKEEEHKEEEHKSKEHKSKGKKDKGKKDKGKHKKAKKEKVKKHVVKNVIEDE
DKDGVEIINLEDKEACEEQHITVESRPLSQPQCKLIDEPEQLTLMDKSKVEEKNLSIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(40204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="potential splice acceptor sequence"
complement(40204. .40209)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="potential splice donor sequence, aag/gtaaca"
join(45401. .46396,46562. .50233)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="garp"
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                                                                                                                                                                                                                                                                                                                                                                             source
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Consensus quality: 200455 bases at least Q40
Consensus quality: 201365 bases at least Q20
Consensus quality: 201775 bases at least Q20
Insert size: 202045; sum-of-contigs
Insert size: 161399; 19.6% error; agarose-fp
Ouality coverage: 6.15x in Q20 bases; sum-of-contigs Quality
coverage: 7.70x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 7, 2001 this sequence version replaced gi:13396737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
------ Project Information
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Center code: SC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: bA469E8
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8084 16795: contig of 7983 bp in length
16796 16895: gap of 100 bp
16896 73805: contig of 56910 bp in length
73806 73905: gap of 100 bp
73906 147587: contig of 7266
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178902 179001:
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                                           fragment_
16896..7
                                                                                                                                      vector_side:left"
                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/note="assembly_fragment:01698
fragment_chain:1"
                                                                                                                                                                clone_end:SP6
                                                                           /note="assembly_fragment:01844
fragment chain:1"
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                                                                                                                                                                                                     note="assembly_fragment:00874
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202645: contig of 21026 bp in length
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Waterston, R.H.
                                                                                                                                               AC096550 AC013666
AC096550.1 GI:15638715
                                                                                                                                                                                       AC096550 181486 bp
Homo sapiens chromosome 2 clone
                       Unpublished
                                       The sequence of Homo sapiens clone
                                                    Waterston, R.H.
                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                Mammalia; Eutheria; Primates; lacks (bases 1 to 181486)
                                                                                                           Homo sapiens
                                                                                                                                   HTG; HTGS_PHASE1; HTGS_DRAFT
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clone_end:T7
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fragment_chain:1"
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              to 181486)
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Assembly program: Phrap; version 0.990319
Consensus quality: 176334 bases at least Q40
Consensus quality: 178430 bases at least Q30
Consensus quality: 179303 bases at least Q20
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Submitted (18-SEP-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Sep 18, 2001 this sequence version replaced gi:7382143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
------ Project Information ------
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                                                  clone_end:SP6
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                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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                                                                                            /note="assembly_name:Contig7"
                                                                                                                                                             /note="assembly_name:Contig5"
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                                                                                                                                                                                                                              /note="assembly_name:Contig3"
                                                                                                                                                                                                                                                                                              'clone="RP11-20F13"
                                                                                                                             note="assembly_name:Contig6"
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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gardner,M.J., Tettelin,H., Carucci,D.J., Cummings,L.M., Aravind,L., Koonin,E.V., Shallom,S., Mason,T., Yu,K., Fujii,C., Pederson,J., Shen,K., Jing,J., Aston,C., Larz, Schwartz,D.C., Pertea,M., Salzberg,S., Zhou,L., Sutton,G.G., Clayton,R., White,O., Smith,H.O., Fraser,C.M., Hoffman,S.L. et al. Chromosome 2 sequence of the human malaria parasite Plasmodium
      Direct Submission
Submitted (02-NOV-1998) The Institute for Genomic Research,
Medical Center Drive, Rockville, MD 20814, USA
                                                                                                   Erratum:[[published erratum 4;282(5395):1827]]
2 (bases 1 to 14867)
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Science 282 (5391), 1126-1132 (1998)
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Center Drive, Rockvi
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NRNSVKKYKOTY IYILNDLSFYKYIKNNDRTKKKNFFLLSSSMKELIGKNILSVSN
RYIKHLHEEDNEDQKDQYVCSLTFLNLFFDKI IHPHYI YNLMCHVYKTYNYFKOKL
INEDIISLLLTCSKFQYFIENNSNDRYCRKELIHLKYNIIDDLIKNYLNTYKSISID
NISKLFISLSNSKYTCEVNENLLLESLQSEFEKVTKTSKKGTHMMDNNILDNNNSCE
KYEHRYIEYKKENLFINLNKIIECLIKLNIFUYLKKKKTYLYLYKQSLCPINLKENIL
KKILYIANNLYMYEMYGYVCEMLERVLSSHKEQNLFSYNYNKNVEHKMFDKILCHISE
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FILNKIIDKNFILFYECLLKILLNIKFVNFQSLCISLISLKNIYYNILRNNYYIVNNV
LFNDIMKFSLYLCNIFLGKRIKTENENAVLIIHNNDQTNYSNKENIKDIIIQKRIKEY
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GLKKGSLKSKTRKSTSGSKFKPLNKYFLSKIKIVTSLNKIPSPLKEQKNTEVNLPESL
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DNFKGRTGSFGSRVFDNRKGSFKKRFISNRNKSSVKSYRGNGSNKMGRKSFNKAPTSR
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/gene="PFB0490c"
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/gene="PFB0490c"
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/protein_id="AAC71888.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="PFB0495w"
11241. .14606
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/protein_id="AAC71887.1"
/db_xref="GI:3845198"
/translation="MKEKNEKIMDYLSCPLDDVVDREKKSGKNSLLKSSSTKKSDYKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDY I EMSNTMY VLFY DY LKNINSERQSNILRNNSTNDRFIDEIKEKKY KLNNNTLIKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="predicted by GlimmerM"
/codon_start=1
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/db_xref="taxon:5833"
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TITLE
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Davy-Carroll, L. Dedgado, O.,
Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Dedgado, O.,
Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H.,
Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C.,
Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J.,
Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T.,
Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunarathe, P., Hale, S.,
Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A.,
Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C.,
Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J.,
Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
Joudah, S., Kratusson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Voulah, S., Kratusson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Lewis, L., Li, J., Li, Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
Loulseged, H., Lozado, R.J., Lucier, A., Lucier, A., Luna, R.,
Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M.,
Martinez, E., Massey, E., Mawhiney, E., Mitchell, T., Mohabbat, K.,
Morgan, A., Mayuen, N., Miner, Z., Mitchell, T., Mohabbat, K.,
Morgan, A., Mayuen, N., Neal, D., Newtson, J., Newtson, N.,
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Peery, J., Peters, L., Pickens, P., Primus, E., Pu, L., L.,
Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M.,
Stone, H., Sutton, A., Stantk, A., Tamerisa, K.,
Stone, H., Sutton, A., Stoner, S., Sonakk, A., Tamerisa, K.,
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Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R. Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Walliams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D. Weinstock, G. and Gibbs, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens chromosome Xp clone RP11-707P20, SEQUENCE, 2 unordered pieces.
Direct Submission
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(bases 1 to 189214)
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                                                                                                   Submitted (12-JUL-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baylor Plaza, Houston, TX 77030, USA on Nov 29, 2001 this sequence version replaced gi:16327947.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57784
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130944
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Consensus quality: 190931 bases at least Q40
Consensus quality: 191911 bases at least Q30
Consensus quality: 192818 bases at least Q20
Estimated insert size: 190344; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 17.7x in Q20 bases; sum-of-contigs est:
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Center clone name: RP11-707P20
Center clone name: RP11-707P20
Sequencing vector: Plasmid; M77789
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Location/Qualifiers
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Garcia, A., Hogues, M., Holloway, C., Hollins, B., Harrim, Havlak, P., Hawes, A., Hennandez, J., Hernandez, J., Howard, S., Hume, J., Jackson, L.E., Homsi, F., Howard, S., Hart, M., Holloway, C., Hollins, B., Hernandez, J., Jackson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Kvar, C., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratlsson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Louiseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Laz, L., Lucier, A., Lucier, R., Luna, R., Ma, J., Laz, L., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Massey, E., Mawhiney, E., Nockenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Nortens, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., 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Homo sapiens chromosome Xp clone RP11-539J11, WORKING DRAFT
SEQUENCE, 3 unordered pieces.
AC108683
                            Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H. Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williamson, A., Wleczyk, R., Wooden, S., Wolliamson, A., Wleczyk, R., Wooden, S., Wolf, Wu, Y., F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.)
NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as soon as it is available and the accession number will be preserved.
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Sequencing vector: Plasmid; M77789
Chemistry: Dye-terminator Big Dye: 100% of reads
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/
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/organism="Homo sapiens"
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3 171642: gap of unknown length
13 196472: contig of 24830 bp in length
73 196572: gap of unknown length
73 208319: contig of 11747 bp in length
14 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aacctaatcaaattaatatcttatgtgatataatttagaaatataaatgattaaccttta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86827 bp DNA linear INV 04-MAY Plasmodium falciparum MAL3P5, complete sequence. AL034556 AL008971 AL008972 AL008978 AL010141 AL010153 AL010162 AL010206 AL010210 AL139179 AL034556.3 GI:7711064 HTG; Centromore.
                                                                                                                                                                                                                                                                                                                                       CR10 1SA, UK
CR10 1SA, UK
On May 14, 2001 this sequence version replaced gi:2982535
gi:2982536 gi:2894454 gi:2982554 gi:2982562 gi:2894489 gi
gi:2982574 gi:4493931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bowman,S., Lawson,D., Basham,D., Brown,D., Chillingworth,T., Churcher,C.M., Craig,A., Davies,R.M., Devlin,K., Feltwell,T., Gentles,S., Gwilliam,R., Hamlin,N., Harris,D., Holrod,S., Hornsby,T., Horrocks,P., Jagels,K., Jassal,B., Kyes,S., McLean,J., Moule,S., Mungall,K., Murphy,L., Oliver,K., Quail,M.A., Rajandream,M.-A., Rutter,S., Skelton,J., Squares,R., Squares,S., Sulston,J.E., Whitehead,S., Woodward,J.R., Newbold,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission Submitted (17-DEC-1998) P.falciparum Genome Sequencing Consortium,
                                                                                                                                                                                                                                                                                                see
                                                                                                                                                                                                                                                                                                                                                                                                                               The Sanger Centre, Wellcome Trust Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barrell, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bowman, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The complete nucleotide sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   malaria parasite P. falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG; centromere; CTRP protein; initiation Serine/threonine protein phosphatase.
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                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/Projects/P_falciparum.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  more information about this sequence or the Malaria Project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ., Skelton,J.,
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                                                                                                                                                                                                                                                    .86827
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ISNNEINIKKLNQSDEDINITSDLIYERLEFTKVLWYIQKIEYLKFKYQYDIINEQ
YPIIKNEKTYLDLLNYGYKIVMSPDVDNSLFEKTKIDSIPNEKDKNNQMENQKNSKNY
                                                                                                                                                                                                                                                                                                                                                                 DQKKDILKKIYFLKGNKLDDIQILNELYVMIYMRLLFECSLKLISIKKNIHLLEKKME
FDKDNKIIYLMSADYMNULRRNILKRESKNEERENINSFASFPFLJGKNIIYFEDEIG
RSRDNTIYNNYDKEINKTTTNNNNNDNDNDLGSNNDHIGSNNDHIGSNNDHIGSNNDHIGSN
NNNNICSNNNNNICSNNNNNICSNNNNNICSNNDKFRFEKEKRKI
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NNNIVMGDIKNNNIFYKKYNLFESSIISYFYIKDIYEYNYKLRLYYIYDNLLKKFCR
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1097 aa, possible signal sequence, predicted using
hexExon"
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complement/??"
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join(7669. .7717,7800. .7829,7912. .7940,8064. .8106,

8302. .8368.8568. .8641,8713. .8812,8924. .9006,9122.

9369. .9505,9613. .9838)

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FYDHINSSSNRCSFKNLKKQQTDDNTKHIIMGKEKYPMKSDHEKKNNNICGNINIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIKKIRIHNKCSYIPLLFLNIYDSYIYKNKILRWLPKFRKRRKDKEBYYYITOMVRK
KRREAJKYNEISDEQNLFNKEYIYEIYLEYSIKYGILSPHLSLIYILKNISEBCVNIYC
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KNTNISSYSTYNNMEKENINIYDKYNIHNFYTEKSISYKDENCOHITLNMIYLLNOTY
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/note="predicted splice acceptor sequence for (revised of PFC0575w)"
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/note="predicted splice donor sequence
PFC0575w (revised)"
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IDIVKFKDLYYCMINNINNIESYIHKVDHNECVYRIEKAVNKILYEYWYLNEKENIY
YKNKIKKYLFYLNNISISDLYYNISSYNKIYNGNKYKNKNESHIEYSLKUDIHLLE
LYTQRIQNCCDIFSYIYKKYNFNEKNPFLNYLYYELHYIVYSEKKKKKKFFSFISSSP
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/note="predicted splice dor
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                                                                                                                                                                                                                                         MVVCGPKT'
                                                                                                                                                                                                                                                            YSYDTMVNSFTFSYFFFSLSYLLFILFYHPDMYASYIFFKTLTYSGLPTYYYSLYNNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MLGLKRKNVFYLLVSVPSLFAYFLKRHKDNENNYETLINNNDIE/
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PFC0581w"
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PFC0581w"
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PFC0581w"
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PFC0581w"
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PFC0581w"
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/translation="wkkkkkhyfsikfynvdknkyvlcskdyiriinymiglhifrll OkifhiyfaneQiassffeshknyrvtkediidgiekcwfnitdylisesikodndfs NDIKTTVTAMKNKMDQLLTTSYSNKKIDTVNASFQWAQSPEYIFLNIKFSHRWSSPGA LKVKDEEIVSKKNNFSFSALSNDSNSYTKKYIVDLTLLDNIIESETKYWFASVCKVVV QNFLKEEKNNSDKLQDDIDEDEEKYFDEEILREAKKKSEEYDKDDEEL" TLKKEKKKIWNRLLLSKEKYPNMQVWWDMKEKRIHIITFVTINLFFLLSLSHRYHDSV /codon_start=1 /product="hypothetical protein, PFC0581w" /protein_id="CAB90285.1" /db_xref="GI:7711066" acceptor sequence for exon 2 of

donor sequence for exon Ν of

acceptor sequence acceptor sequence donor sequence for for for exon exon exon 4 w of of.

acceptor sequence sequence for for exon exon 4 of ហ of.

acceptor donor sequence sequence for for exon exon 5 of 6 of

donor sequence for exon δ of

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donor sequence for exon 7 of

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Drive, Walnut Creek, CA 94598, USA
On Jan 30, 2002 this sequence version replaced gi:15290376.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
                                                                                              Submitted (23-MAR-2000) Production Sequencing Facility, Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA (bases 1 to 192731)
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Mammalla; Eutheria; Primates;
1 (bases 1 to 192731)
DOE Joint Genome Institute and
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AAQ78892	AAC58017	ABL34155	AAS46505	ABL33267	AAK86271	ABL33141	ABL32129	AAS46646	AAH93026	AAN60472	AAS61427	ABL33703	AAX58642	AAS61074	ABL32323	ABL33019	AAF12929	ABL32255	ABL33667	ABL32142	ABL33545	AAS61077	ABL32326	AAS61426	AAS61276	ABL33534	ABL33569	ABL32257	AAH93026	AAK86270	ABL32487	ABL34255	ABL34175	ABL33451	AAK82710
	Arachidonic acid m	Human immune syste	Tumour suppressor	Human immune syste	Human immune/haema	Human immune syste	Human immune syste	Tumour suppressor	Human inflammatory	Sequence encoding	_	Human immune syste			Human immune syste	Human immune syste	Aspergillus oryzae	Human immune syste	Human immune syste		Human immune syste	Human gene regulat	immu		gene re	immune	immune	-	Human inflammatory	immune,	immune	Human immune syste	Human immune syste	Human immune syste	Human immune/haema

ALIGNMENTS

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RESULT
AAX58644
Aspen; 4-coumarate coenzyme A ligase; lignin; transgenic plant; tree; conifer; forestry; Pt4CL1; promoter; xylem; ss.
      12-NOV-1998;
                                                                misc_feature
                                                                                      misc_feature
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                                                                                                                    Key
                                                                                                                                                                       Aspen 4-coumarate coenzyme A ligase Pt4CL1 gene promoter
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                                   WO9924561-A2
                                                                                                                                   Populus tremuloides
                     20-MAY-1999.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheiner's disease, ALDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
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 Human immune
                                                                                                                 ABL34073 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7602
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les 238; Conser
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                                                                                                                                                                                                              ACTTTTTTATAAAACAT 7346
                                                                                                                                                                                                                                cctaattgttaaaatat 705
                                                                                                                                                                                                                                                                                      ATATATTACCTTAAAATTCTATATTAAATTTATTTTTTATAAAACATTAAAACTAACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tcaaactggccaggacaattattaaaattaattattattttttctaataaagcactt 688
                                                                                                                                                                                                                                                                                                                                                               ТАРАСТАРТАРАТ В ТАРАТ В ТАРАТ В ТЕТЕТ 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aaacctaatcaaattaatatcttatgtgatataatttagaaatataaatgattaaccttt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9155 BP; 2719 A; 122 C; 1814 G; 4500 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Piepenbrock
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system associated gene SEQ ID NO:
                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence is a gene of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprising fragment of chemically modified and treatment of diseases associated with
                                                                                                                 DNA;
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                                                                                                                 40862
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                                                                                                                 ВÞ
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ytosines. The s
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abnormal
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genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with cytosine methylation \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 40862 BP; 14301 A; 414 C; 7426 G; 18721 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention provides a number of human
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                              ttggatttgaatgaactcaattacatcacaaaaaacctaatcaaattaatatcttatgtg 536
                                                                                                                                            gttatgtgtt--aaatataattgtaaattattattataatataataaaatttaaagttttat 12990
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                                                                                                                                                                                                                                                                                                                                                                                          gaccagttgtcaaatgaccactcgacttggggcatggtgatttttcaaaatcacaactcaa 356
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1; SEQ ID NO 2046; 32pp + Sequence Listing; German.
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2000DE-1043826
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Pred. No. 0.00039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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06-APR-2000;
07-APR-2000;
30-JUN-2000;
01-SEP-2000;
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                    The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequen ($$) and sequences complementary to ($$). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation st and/or single nucleotide polymorphisms and also to be used in an exercise of the cytosine methylation stand/or single nucleotide polymorphisms and also to be used in an
                                                                                                                                                                                                                 Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for
         array for analysing diseases associated with CpG dinucleotides
                                                                                                                                                                                            analysing
cancer -
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                                                                                                                                                                                                                                                                                  Piepenbrock
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                                                                                                                                                                                                 oncogenes, useful in designing primers and probes diseases associated with cytosine methylation stat
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2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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probes
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 also
 be used
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            e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                      soybean genome which are associated with soybean cyst nematode (SCN) resistance. The nucleic acids are used to transform plants, and can produce soybean plants having an rhgl or an Rhg4 SCN resistant allele. The nucleic acids can be used for investigating rhgl or Rhg4 haplotypes of soybean plants and for introgressing SCN resistance or partial SCN resistance into soybean plants. They can also be used in plant breeding programmes. The invention also relates to proteins encoded by such nucleic acid molecules, as well as antibodies capable of recognising these proteins. The present sequence is a nucleic acid molecule
                                                                                                                                                                                      Claim
                                                                                                                                                                                                           New purified nucleic acid for producing a soybean plant having soybean cyst nematode resistance and for use in plant breeding programs - \,
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Sequence 513445 BP; 173367 A; 85402 C; 83912 G; 170492 T;

272 other;

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ABL32058/c
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                                                                                                                                                                                                                                                                                                                                                                                         antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
30-JUN-2000;
                                                       02-JUL-2001;
                                                                                                              03-JAN-2002
                                                                                                                                                                                                                                                                                                              neurofibromatosis;
                                                                                                                                                                                                                                                                                                                                        antiinflammatory; cancer; eye disease; arterioscler
acute myeloid leukaemia; Alzheimer's disease; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL32058 standard; DNA;
                                                                                                                                                                        WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immune sýstem associated gene SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL32058;
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                                                       2001WO-EP07537
2000DE-1032529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                 rheumatoid
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47.9%;
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                                                                                                                                                                                                                                                                                                           arthritis; psoriasis;
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                                                                                                                                                                                                                                                                                                           bowel disease;
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genes which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
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diagnosis and treatment
osine methylation -
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TAATTCCAACAATAATATATTTTTTA
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                                                      CATTACATATTATAACATATTACATATCATATTTCAATATATCATTTCTAATTTAAAT
                                                                                                                             TTCTATACATTCTTTTTAAAAATATTTTAAAAATAACTTATTTCCACTATAATTCAATATA 5241
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                                                                                                                                                                                                                                                                                            TCTTCTAAATCAAATCCTCTCATAAAACTTTCATCAAACTTAACTTTCTTATATTCACAA 5479
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                                                                                                                                                                                                                        ATTATCGCTTTACCGCAAATATCTTTAATATAAAAAA --TAAACACTTCATAAATACAAA 5301
                                                                                                                                                                                                                                                                              CTTAATAAAAAACATTTCTAACTTTAACTTTACAAATTAATCATAATTAACTTAAAATAA
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47.48;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides a number of human immune system associa genes which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal cytosine methylation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JUL-2001; 2001WO-EP07537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiarteriosci
  646
                                                                                                                                            531
                                                                                                                                                                         468
                                                                                                                                                                                                     591
                                                                                                                                                                                                                                                                                      348
                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                   tatcttatgtgatataatttagaaatataaatgattaacctttaaatctcgagtttctct
                                                                                                                                            tcacgggttggctaatcaattattaattaaatgatagtatttttgataatttaatt
                                                                                                                                                                                                                                                         acaactcaatttgaaaactaaaattaaaaaagatttagattattaaattattaggttaat
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attattaaaattaattattattttttctaataaagcacttcctaattgttaaaatat
                                                                                                                                                                      aaaaatttattggatttgaatgaactcaattacatc--acaaaaaacctaatcaaattaa
                                                                                                                                                                                                   tataaaaaacacgtataattgggctagatttaacagctattattcaaactggccaggaca
                                                                                    AACTTTATCTCTTATAAATAAAATAAAAAAAAAAACAAAAATTTAAATTTTAATTATATAA
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                                                                                                                                                                                                                                                                                                                                                                                        6071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 298;
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                                                                                                                                                                                                                                                                                                                   Conservative
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2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                       BP; 1973 A; 46 C;
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48.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Berlin
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                                                                                                                                                                                                                                                                                                              Score 69; DB 24;
Pred. No. 0.0013;
0; Mismatches 26
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RESULT 9
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The invention relates to 224 nucleic acid sequences comprising at least 18 bases of a chemically pretreated gene associated with gene regulation selected from 43 known genes (or complementary sequences). The chemical pretreatment converts cytosine bases unmethylated at the 5-position to uracil or another base with hybridisation behaviour dissimilar to cytosine, to enable analysis of cytosine methylations. The DNA sequences, oligomers (or sets/arrays) and method are useful in the diagnosis of diseases (or predisposition to diseases) associated with gene regulation and in therapy of such diseases, by enabling analysis of the cytosine methylation patterns of such genes, kits are provided. They are especially useful in diagnosis and therapy of e.g. severe combined immunodeficiency disease, cardiac disorders, haemophilia, solid tumours and cancer, Werner syndrome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cardiac damage; inflammatory response; Haemophilia; Werner syncasthma; HDR syndrome; congenital heart defect; Saethre-Chotzen renal disease; Preeclampsia; cardiac allograft vascular disease
                                                                                                                                                                                                                                                                New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficien
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07-APR-2000;
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                                                                                                                                                                                                                     Claim 1;
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nephrotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour;
immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human gene regulation-associated gene oligonucleotide #31.
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                                                                                                                                                                                                                                                                                                                                                                                        (EPIG-)
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                                                                                                                                                                                                                                                                                                                                                          Piepenbrock C,
                                                                                                                                                                                                                                                              regulation, and therapy
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2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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RESULT 10
AAK82710/c
ID AAK827
XX AAK827
XX AAK827
XX O7-NOV
DT 07-NOV
XX
DE Human
XX Human;
KW Cytost
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Cytost
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PN W02001
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PD 09-AUG
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PF 17-JAN
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     17-JAN-2001; 2001WO-US01354
                             09-AUG-2001
                                                                                                      cytostatic;
                                                                                                                                                                      07-NOV-2001
                                                                                                                                                                                                                   710/c
AAK82710 standard;
                                                     WO200157182-A2
                                                                                                                     Human;
                                                                                                                                          Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37522
                                                                                                                                                                                               AAK82710
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                                                                                                                  immune; haematopoietic; immune/haematopoietic antigen; cancer;
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                                                                                                      gene
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                                                                                                     therapy; vaccine; metastasis;
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14-AUG-2000
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12-MAR-2000

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19-MAY-2000

07-JUN-2000

28-JUN-2000

07-JUL-2000

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07-JUL-2000
2000US - 0231414
2000US - 0231244
2000US - 02311413
2000US - 0231414
2000US - 0231414
2000US - 023298
2000US - 023298
2000US - 023239
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2000US - 023239
2000US - 023240
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2000US - 023363
2000US - 023421
2000US - 0234224
2000US - 023423
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2000US - 0236367
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2000US-0227182.

2000US-0227182.

2000US-0227109.

2000US-022924.

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2000US-0225270.
2000US-0225447.
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2000US-022964
2000US-0224518
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2000US-0180628.
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2000US-0184664
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01-NOV-2000

08-NOV-2000

01-NOV-2000

01-NO
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01-DEC-2000
01-DEC-2000
05-DEC-2000
06-DEC-2000
08-DEC-2000
08-DEC-2000
08-DEC-2000
 Nucleic acids encoding useful for preventing,
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2000US-0246609.

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2000US-0246613.
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2000US-0241221.
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human immune/hematopoietic antigen diagnosing and/or treating cancers
                                                                                                MS
   polypeptides, and
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RESULT 11
ABL33451/c
ID ABL334
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AC ABL334
XX
DT 26-MAR
DT 26-MAR
XX
KW Human;
KW Human;
KW antiar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic antigen genomic CC sequences from the present invention. AAK54942 to AAK95950 and AAM82169 CC careers to be present invention. AAK54942 to AAK95950 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                 Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemiac; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                               ABL33451
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                                                                                          Human
                                                                                                                      26-MAR-2002
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                                                                                                                                                                                                                                                                                                                  immune
                                                                                                                                                                               standard;
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                                                                                        system
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48.2%;
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                                                                                                                                                                               DNA;
                                                                                          associated
                                                                                                                    entry)
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Pred. No. 0.0015;
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                                                                                                                                                                               ВP
                                                                                       gene
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                                                                                          SEQ
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                                                                                          <u>N</u>O::
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cytostatic
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antiinflammatory;

cancer;

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arteriosclerosis; anaemia;

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Best Local S
Matches 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                   2194
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
2134 TATTACCCATACTAAAATACAATAATCTTAA
                                                                                                     2251
                                                                                                                                                                                                           2370
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19787 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUL-2001;
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                         696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention provides a number of human immune system associated
                       gttaaaatatatgtctaaacactaataataa 726
                                                                                                    CTATTTTCATATATACACTTAAAAATAACCTA--
                                                                                                                   2002-130909/17
                                                  TTCATTATCAATAAAAAATAATATTTTTATTTTTTTTTCTCAAACAAAATCTTAATC
                                                                          ggccaggaçaattattaaaattaattattattttttctaataaagcacttcctaatt
                                                                                                                                                      CCAAAATAACGATATTTCGTAATTAAAAATTAAAAAACTCATTA-TAACTATTTTTCCTC
                                                                                                                                                                                atcaaattaatatcttatgtgatataatttagaaatataaatgattaacctttaaatctc
                                                                                                                                                                                                          gataatttaattaaattttattggatttgaatgaactcaattacatcacaaaaaaccta
                                                                                                                                                                                                                                                            TCTAATTATAATTTAACATTTCAACTAAAAATAACTTAAAAATTCAATAAAACTATTTCA
                                                                                                                                                                                                                                                                                   203;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 1424; 32pp + Sequence Listing; German
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                                                                                                                                                                                                                                                                                                                                                                  Conservative
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.2000DE-1043826
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Pred. No. 0.0016
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                                                                                                                                                                                                                                                                                                                                                                                         DB 24;
                                                                                                                                                                                                                                                                                                                                                                  184;
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RESULT

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ABL34175/c
ID ABL341
XX ABL341
XX ABL341
XX ABL341
XX ABL341
DT 26-MAR
XX Human;
KW Human;
KW antiar
KW neurop
KW antirh
KW antirh
KW acute
KW neurof
KW acute
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Conservative
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24968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurofibromatosis; rheumatoid arthritis; psoriasis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL34175 standard; DNA; 113515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 113515 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid comprising fragment of chemically modified gene,
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                                                  390
                                                                                                                                                                                                                                                                      270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis and treatment of diseases associated with osine methylation
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                                                                                                                                                                                                                                                                                                                         ATATTACTTTATAAACAATAATCCAAATATAAAAAATTAAAAATTAACACAAACAATTT
                                                                                                                                                                                                              atagattaaaacagctcaatgtgaggtgaccagttgtcaaatgaccactcgacttggggc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 2148; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Piepenbrock C,
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2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35172 A; 1174 C;
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48.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berlin
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Pred.
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No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22520 G; 54649 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            .0017;
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                                          Query Match
Best Local S
Matches 224
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                                                                                                                                  The present invention provides a number of human immune system associate genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcrative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antirheumatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzhelmer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUL-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                         cytosine
                                                                                                                                                                                                                                                                                                    Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                             WPI; 2002-130909/17.
                                                                                                             Sequence
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                 87
                                            Local Similarity
les 224; Conserv
                                                                                                                                                                                                                                                                                      diagnosis and tre
osine methylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                              10191
                                                                                                                                                                                                                                                            SEQ ID NO 2228; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                       Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                             2000DE-1032529
2000DE-1043826
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                                                                                                                                                                                                                                                                                                   and treatment
                                                                                                             ВP;
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                                                                                                             2964 A;
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                                                     5.8%;
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                                                                                                                                                                                                                                                                                                                                                                        Berlin
                                                                                                             285 C;
                                            0;
                                         Score 67.4; DB 24;
Pred. No. 0.0026;
0; Mismatches 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene SEQ ID NO:
                                                                                                           2323 G;
                                                                                                             4617
                                                                                                             T; 2
                                          Indels
                                                                 Length
                                                                                                             other;
                                                                     10191
                                          0;
                                                                                                                                                                                                                                                                                                                 useful
                                                                                                                                                                                                                                    associated
                                          Gaps
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RESULT 14
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ABL32487
                                                                                                                                                                                                                                                             Human; immune system disease; cytosine methylation; antiasthy antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; anti-HiV; anticonvulsant; ophthalmological; antitheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anacacute myeloid leukaemia; Alzheimer; disease; AIDS; epilepsy, acute myeloid leukaemia; Alzheimer; disease; AIDS; epilepsy
                                                                                                        30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                   Human immune system associated
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                                                                                                                                           02-JUL-2001;
                                                                                                                                                                   03-JAN-2002
                                                                                                                                                                                           WO200200928-A2
                                                                                                                                                                                                                                         gene;
                                                                                                                                                                                                                                                       neurofibromatosis;
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                                                                                 (EPIG-)
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                                                                                                                                                                                                                  sapiens.
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                                                                                 EPIGENOMICS
                                                         Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                          standard; DNA; 17183
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                                                                                                        2000DE-1032529
2000DE-1043826
                                                                                                                                             2001WO-EP07537
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                                                                                                                                                                                                                                                                             anaemia;
                                                                                                                                                                                                                                                       disease;
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Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with

gene, useful abnormal

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RESULT 1
AAK86270
ID AAK8
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Best Local Similarity
Matches 197; Conserv
    31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
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                                                                                17-JAN-2001; 2001WO-US01354.
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                                                                                                                                                               WO200157182-A2
                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                 Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41082
                                                                                                                                                                                                                                                                                                                                            07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                         AAK86270 standard; DNA;
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ine; metastasis; ds.
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Nucleic acids encoding useful for preventing,
preventing,
        human immune/hematopoietic diagnosing and/or treating
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cancers
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Search completed: July 30, Job time: 4595 sec

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis at treatment of diseases associated with inappropriate (I) expression. For
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AL069440 Drosophil
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6.2	6.2	6.2	6.3	6.3	6.3	6.3	6.3	6. ₃	6.3	6.3	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.5								6.6	
1001	1101	987	905	1101	1101	928	996	798	1101	1027	307	1203	876	1190	1085	1101	734	886	886	1101	1092	1225	928	1101	1143	1143	1101
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CNS0155H	CNS003BD	CNS014PQ	CNS00KHX	CNS00LT2	CNS004ZW	CNS00DKY	CNS00FUH	AI909641	CNS00FYG	CNS02T50	CNS00A3W	CNS015WU	CNS009G1	CNS020N7	CNS016YR	CNS00EQL	CNS010MP	CNS07JUX	вн177277	CNS00B01	CNS020K7	CNS0161D	CNS00DKY	CNS001FB	AL565457	AL565457	CNS00EQL
AL105023 Drosophil	AL064091 Drosophil	AL104456 Drosophil	AL077798 Drosophil	AL078714 Drosophil	AL055440 Drosophil	AL071865 Drosophil	AL071063 Drosophil	AI909641 PM-BT217-	AL071206 Drosophil	AL212733 Tetraodon	AL054893 Drosophil	AL106008 Drosophil	AL053529 Drosophil		AL107373 Drosophil	AL069526 Drosophil	AL099163 Drosophil	AL614235 T3 end of	вн177277 008_L_22-	AL057419 Drosophil	AL175696 Tetraodon	AL106171 Drosophil	AL071865 Drosophil	AL060732 Drosophil	AL565457 AL565457	➣	AL069526 Drosophil

ALIGNMENTS

RESULT 1 CNS0039G/c

DEFINITION

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REFERENCE
AUTHORS
TITLE
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                                                                                                     source
                                                                                                                                                                                                                                                AL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo.

NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pand have to order individual BAC closes the entire library or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fly), genom
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AL063971
                                                                                                                                                           and how to order individual BAC clones, the entire library, filters for hybridization from the BACPAC Resource Center compand at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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/organism="Drosophila
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
                                                                                                                                Location/Qualifiers
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                    fly), ger
AL069706
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Drosophila melanogaster genome sur
BACR29B23 of RPCI-98 library from
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain 92; on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be contern of the Location/Qualifiers
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Submitted (02-JUN-1999) Genoscope - Centre
BP 191 91006 EVRY cedex - FRANCE (E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNS0039G 1101 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLY), genomic survey sequence.
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                    www.genoscope.cns.fr)
 Location/Qualifiers
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Drosophila melanogaster
                 fruit fly
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                                 ttcaccaaccccgtcctcc 1040
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                                                                                                        ttcaatcaatgttttccctatactacccccccaacaactccataatacccaatttgtcct 1020
                                                                                                                                                   HCHMYHMMHMYMYCCHYYCTCHTHATTHYHYMCTCYHYCTWHTYWTAYWWAWTAHAMTTA
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR08K10"
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                                                                                                                                                                                                                            TTTTTTTTTWMAWAYACAMMAYTWTTTTAWTATTTTTTTTTTTMAATATYCWATATTTTMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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Location/Qualifiers
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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Pred. No. 1.5e-05;
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Human gene number estimate provided by genome wide analysis using
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                                                                                                                                 and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Local Similarity 45.3 hes 184; Conservative
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Drosophila melanogaster genome sur
BACR08K08 of RPCI-98 library from
                                                                                                                                                                                                                                                                                                                                                                               melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BUCP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, Cancer Genetics at the Roswell Park Cancer Institute by partial ECORI digestion of Drosophila DNA provided by the BOCP from the GEORAL GRAPH CANCER CANC
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Eukaryota;
                                                                                                                                                                                                         isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as collaboration with the Berkeley Drosophila Genome Project The BDGP is constructing a physical map of the Drosophila
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Pred. No.
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                                            melanogaster"
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rom Drosophila melanogaster (fruit
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segref@genoscope.cns.fi
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1 (bases 1 to 910)
                                                                     Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut
                                                                                                                                                                                                                Genoscope.

Direct Submission

Direct Submission

Office (16-FEB-2000) Genoscope - Centre

BP 191 91006 EVRY cedex - FRANCE (E-mail:
                                                                                                                                       Direct Submission Submitted (16-FEB-2000) BBMI, Institut Pasteur,
                                                                                                                                                                          Roth, C.W., Brey, P.T., Ke, Z., Collins, F.H.
                                                                                                                                                                                                                                                                                                                                                                                                   AL142826.1 GI:7000944
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AL142826
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(bases 1 to 910)
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/clone="BACR08K08"
/note="end : TET3"
a 120 c 103 g
1. .910
/organism="Anopheles
/strain="PEST"
                                              Location/Qualifiers
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39.2%;
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segref@genoscope.cns.f
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- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a Determination with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                    CNS010MP

Drosophila melanogaster genome survey sequence T7 end of BAC
BACN04L20 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                           Submitted (23-JUL-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                     Drosophila melanogaster
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/clone="06E14"
/clone="NotreDame1"
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/note="end: SP6"
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                                                                                                                                                                                                                                                                                                                                                                         Direct Submission Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a lasscale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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Roest-Crollius, H., J
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/clone_lib="G"
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/note="Genoscope sequence ID : COA
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Pred. No. 0.00013;
4; Mismatches 160;
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Quetier,F., Saurin,W., Bernot,A. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocal Similarity
                 ttattttttctaataaagcacttcctaattgttaaaaatatatgtctaaaacactaataata 725
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AATWITWIAITWATAIWIAININWIAIWITAAATAIAIAIAIGITAAAAAAAAAAAAAAAA
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48
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
/Clone_lib="RPCI-98"
/clone="BACRO8G08"
/clone="BACRO8G08"
/note="end: T7"
/note="end: T7"
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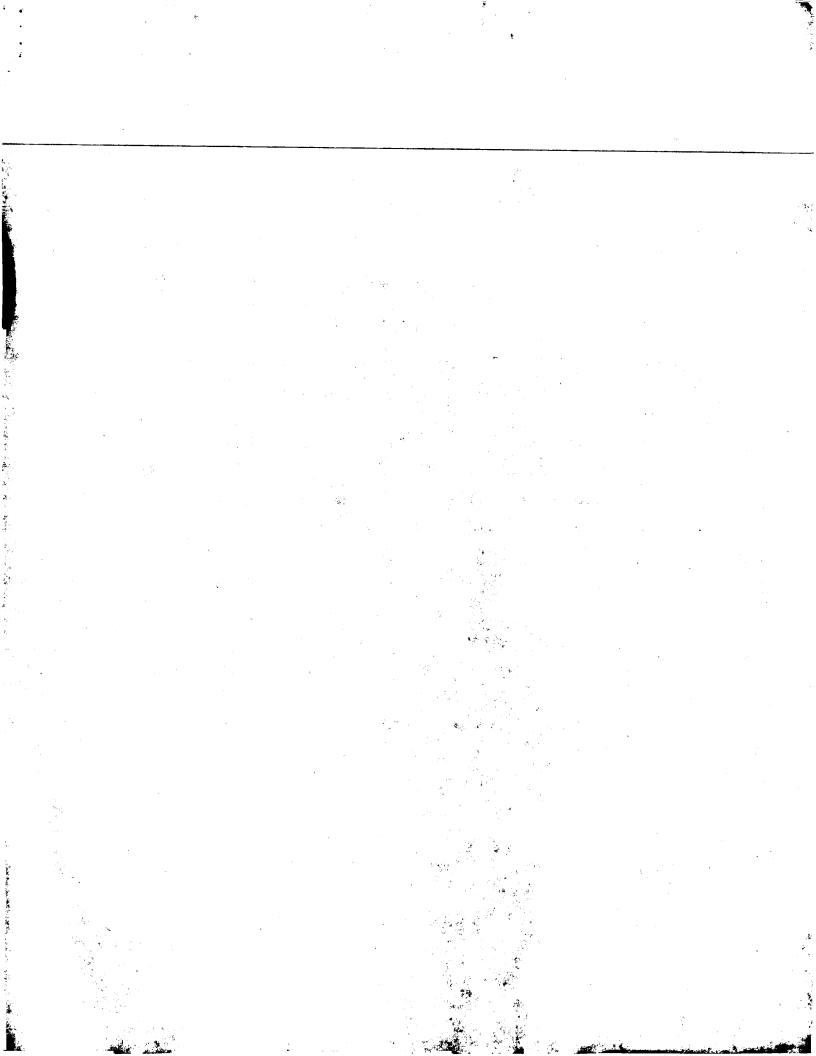
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                                                     atcaaattaatatcttatgtgatataatttagaaatataaatgattaacctttaaatctc
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101H21 of
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Roest-Crollius,H., Jaillon,O., Dasilva,C., Boune Bernot,A., Fizames,C., Wincker,P., Brottler,P., Saurin,W. and Weissenbach,J.
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1 (bases 1 to 945)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human gene number estimate provided Tetraodon nigroviridis DNA sequence
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/db_xref="taxon:99883"
/clone="101H21"
/clone="10-"G"
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                                                                                                                                                                                                                                                                                                                                                                                                              The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be
                                                               aaatcacaactcaatttgaaaactaaaattaaaaaaagatttagattattagattattagg 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ttaattcacgggttggctaatcaattattattaattaaaacgatagtatttttgataatt 462
                                        AARRAAAWRTAWAWAWAATAAAKWKWRWAWRAAWWDWGATGDTWTADWGDADDRRAADR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATAAAAAAAAAAAAAAATWTTAAAAAAAATAAAAAATAT 945
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Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR08110 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determination of this BAC-end sequence was carried out as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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AL063926
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/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                    acaggtggaggacaagccacctctctcaagtcaaaaggccatttcacaaaccaaacccaaat 875
                                                                                                                                                                                                                                                                                                                                                                                          gctgacaaataaattagtgcata-----aaatataatggattggtggtctgtgaaaag 815
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                             atatcagcaggaat 1069
                                                                     CMCCAACCCACATMCMACMCCCMMMTTMAACCAAATMAMAAAACCMTMMAACTCAAMMCC
                                                                                                                                          MTMAMMMCCAMMMMMCMCMAMACNANCTMACAAMCCAMCCCACACMCCCMMACACMCMACA 408
                                                                                                                                                                                                               KRGGWRGGRKTKKVTTMMVRTGCGCCCCCMAKAKTTSGCCBTBTYCMMMAAACNCCMCMA 468
                                                                                                                                                                                                                                             gggaacccaccaccgttccccgccattaaaatccctaatctcaccaacccaactccacag 935
                                                                                                                                                                                                                                                                                     AAAGKRTGGKKKKKTRTBTRDWNBNAHAAATMWNAATBMTGTGKSWMMMATMDMTMTMKG
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Search completed: July 30, Job time: 5471 sec 2002, 10:38:02



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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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                                               GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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US-08-998-416-288
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US-08-998-416-186
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US-08-107-755A-32

US-08-544-332-32

US-07-991-8678-8
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Sequence 1137, Ap
Sequence 36, Appl
Sequence 32, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 15, Appl
Sequence 288, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1137, Ap
Sequence 186, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 186, Appl
Sequence 534, Appl
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US-08-998-416-1137
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52	52	52	52.2	52.2	52.4	52.4	52.8	53	53.4	53.4	53.4	53.4	53.6	53.6	54	54.6	54.6	
4.4	4.4	4.4	4.5	4.5	4.5	4.5	5	5	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.7	4.7	
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US-08-998-416-1036	US-08-998-416-1036	US-08-998-416-683	US-08-319-704-5	US-08-998-416-701	US-08-213-419B-3	US-08-991-677-11	US-08-998-416-595	US-08-998-416-595	US-08-731-722-2	US-08-731-722-2	US-08-731-722-1	US-08-731-722-1	US-08-487-826B-13	US-08-998-416-534	US-08-487-826B-13	US-08-731-722-5	US-08-998-416-191	
Sequence 1036, A	Sequence 1036, Ap	Sequence 683, App	Sequence 5, Appli	Sequence 701, App	Sequence 3, Appli	Sequence 11, Appl	-	Sequence 595, App	Sequence 2, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 13, Appl	Sequence 534, App	Sequence 13, Appl	Sequence 5, Appli	Sequence 191, App	

ALIGNMENTS

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Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philips
APPLICANT: Pohlman
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Sequence 16239264
                                                                                                                                                        TELEPHONE: 919-541-858
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                      FILING DATE: 31-DEC-1996
ATTORIX/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/998, FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                 MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                    LENGTH: 636 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27709
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Steiner, Sabine
Mohr, Christine
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PAG1692RP
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ER: PF/5-30306/A/CGC1976
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US-08-883-795A-36
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Best Local Similarity
Matches 208; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                        APPLICATION NUMBER: US/08/883,795A FILING DATE: 27-JUN-1997 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Gravelle, Micheline NAME: Gravelle, Micheline
                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Recombinant DNA Molecules and Expression TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Delcuve, General APPLICANT: Awang, Gregor
                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
              TELECOMMUNICATION INFORMATION:
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                             REGISTRATION NUMBER: 40,261 REFERENCE/DOCKET NUMBER: 78
                                                                                                                                                                                                                                                                               CITY: Toronto
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 TELEPHONE:
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Pred. No. 3.5e-05;
0; Mismatches 217;
                                                                                                                                                        Version
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RESULT 3
US-07-991-867B-32
; Sequence 32, Application US/07991867B
; Patent No. 5476781
; Patent No. 5476781
; GENERAL INFORMATION:
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IMMEDIATE SOURCE:
CLONE: Rh 32
US-08-883-795A-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                              APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                   453 CATATTTATAAAGTATTTATAATTACATATTTATAAT
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nes 224; Conserv
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                        CITY: Gainesville
STATE: FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36
                                                                            ZIP:
                                                                                        COUNTRY:
                                                                                                                                      STREET:
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                                                                                                                                      E: David R. Saliwanchik
2421 N.W. 41st Street, Suite
                                                                                          USA
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48.8%;
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Pred. No. 3.5e-05;
Prematches 232;
   Version
      #1.
      . 25
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           US-08-107-755A-32; Sequence 32, Application US/08107755A; Patent No. 5721352; GENERAL INFORMATION:
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Best Local Similarity
Matches 205; Conserv
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REFERENCE/DOCKET NUMBER: UF114.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/6 FILING DATE: 19-FEB-1991 ATTORNEY/AGENT INFORMATION: NAME: Sallwanchik, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
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APPLICANT:
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Moyer, Richard W.
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12-DEC-1992
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48.0%;
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Pred. No. 4.2e-05;
0; Mismatches 221;
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Best Local S
Matches 205
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TELEFAX: (904) 372-58 INFORMATION FOR SEQ ID NO:
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APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: NO. 5721352el
NUMBER OF SEQUENCES: 40
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LENGTH: 660 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
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APPLICATION NUMBER: US 0
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION
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PRIOR APPLICATION DATA:
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REGISTRATION NUMBER: 31,79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07 FILING DATE: 30-JAN-1992
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OPERATING SYSTEM:
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                                                            ATAATATCTAAAAATAAATTTGGTAACTTTAATAATGTTTTTCCTATTAGTATAGTTGAG
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2421 N.W. 41st Street, Suite
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Pred. No. 4.2e-05;
0; Mismatches 221;
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Patent No. 5935777
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Best Local
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APPLICANT: Hall, Richard L.
APPLICANT: Gruidd, Michael E.
TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 77
                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H.
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ADDRESSEE: Gerard H. Bencen
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                     369 aattaaaaaagatttagattattaaatttattaggttaattcacgggttggctaatcaatt 428
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CITY: Gainesville
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                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 35
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/657,584 FILING DATE: 19-FEB-1991
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                                                                  Local Similarity
es 205; Conserv
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AATATTAATATATAAAAAAAATTAGTTAATTTAGAAGAATTGCATATAATATATTATGAT 150
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DEDNESS: double
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                                                                     Conservative
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TED: UF114.C4
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                                                                     0;
                                                                  Score 61.4; DB 2;
Pred. No. 4.2e-05;
0; Mismatches 221;
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US-07-991-867B-8
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GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92
FILING DATE: 12-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Moyer, Richard W. APPLICANT: Hall, Richard L. APPLICANT: Gruidl, Michael E. APPLICANT: Gruidl, Michael E. TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression
                                       TELEPHONE: 904-375-8100
                                                                                   FILING DATE: 19-PEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
                                                                                                                                                         APPLICATION NUMBER: US 0: FILING DATE: 30-JAN-1992 PRIOR APPLICATION DATA:
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CTTY: Gainesville
                                                         REFERENCE/DOCKET NUMBER: UF
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                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 12-DEC
                            TELEFAX:
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                            904-372-5800
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                                                                                                                             UMBER: US 07/657,584
19-FEB-1991
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                                                                                                                                                                                                                                                                                                                                                                                FORM:
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Best Local Similarity 48.0%;
Matches 205; Conservative
                                                                                                                                                                                 Sequence 8, Application US/08107755A Patent No. 5721352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
FEATURE:
                                                                                         APPLICANT: Moyer, Richard W.
APPLICANT: Hail, Richard L.
APPLICANT: Gruddl, Michael E.
TITLE OF INVENTION: NO. 5721352el Entomopoxvirus Expression
NUMBER OF SEQUENCES: 40
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                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
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ORIGINAL SOURCE:
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COUNTRY: UZIP: 32606
                                           CITY:
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                              STATE:
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                                                                                                                                                                  INFORMATION:
                                          Gainesville
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Best Local S
Matches 205
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INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                   1122
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REFERENCE/DOCKET NUMBER: UF
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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NAME/KEY:
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LENGTH: 1511 base pairs
TYPE: nucleic acid
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ATTORNEY/AGENT INFORMATION:
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FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
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OPERATING SYSTEM:
SOFTWARE: Patenti
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STRANDEDNESS: double
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attttttctaataaagcacttcctaattgttaaaatatatgtctaaacactaataataaa 727
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                                                 ATAATATCTAAAAATAAATTTGGTAACTTTAATAATGTTTTCCTATTAGTATAGTTGAG
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SYSTEM: PC-DOS/MS-DOS
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19-FEB-1991
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Pred. No. 5e-05;
0; Mismatches 221;
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                                                                                                                                                                                                                                                     TELEFAX: 904-372-5800
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APPLICATION NUMBER: US 08
PRIOR DATE: 19-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/827,685 FILING DATE: 30-JAN-1992 PRIOR APPLICATION DATA:
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ADDRESSEE: Gerard H. Bencen
STREET: 2421 N.W. 41st Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1362 AAAAAAT 1368
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                                                                                                                                                 MOLECULE TYPE: |
ORIGINAL SOURCE:
                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: UF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Bencen, Gerard H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,867
FILING DATE: 07-DEC-1992
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TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 77
                                                                        FEATURE:
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TYPE: n
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LOCATION:
NAME/KEY:
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                                                                                                      NAME/KEY:
                                                                                                                                   ORGANISM:
                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                            LENGTH: 1511 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                        LOCATION:
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complement
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Best Local S
Matches 205
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11,
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                                                                                                                                   CURRENT APPLICATION DATA:
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                                                                  CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
 TELECOMMUNICATION INFORMATION: TELEPHONE: 407-426-7500
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                                                                                                                                            COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palana
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                            NAME: Bencen, Gerard H REGISTRATION NUMBER: 35, REFERENCE/DOCKET NUMBER:
                                                                                                     APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                        STREET:
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205; Conserv
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2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                Li, Y
Hall,
                                                                                                                                                 PatentIn Release #1.0,
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                                                                                                                     US/08/852,629
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Pred. No. 5e-05;
0; Mismatches 221;
                                                                                                                                                   Version
                                                                                                                                                    #1.30
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TELEFAX:

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RESULT 10
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                                                                                                                                                                                 Sequence 15, Application US/08852629
Patent NO. 6106825

GENERAL INFORMATION:
APPLICANT: Moyer, Richard W
APPLICANT: Li, Yi
APPLICANT: Hall, Richard L
TITLE OF INVENTION: VECTOR AND METHOD
NUMBER OF SEQUENCES: 17
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Best Local
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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                                                                             STATE: Flor
COUNTRY: U.
ZIP: 32606
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                                                                                                                     STREET: 2421 N.W. CITY: Gainesville
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Local Similarity 48.0%;
les 205; Conservative
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                                                                                                           Florida
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    Version
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                                                                                                                             Sequence 288, Application US/08998416 Patent No. 6239264
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Best Local :
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                                                                                                                  GENERAL INFORMATION:
                                                            APPLICANT:
APPLICANT:
APPLICANT:
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                                     APPLICANT:
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LENGTH: 4838 base pairs
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ATTORNEY/AGENT INFORMATION:
             TITLE
                          APPLICANT:
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REGISTRATION NUMBER: 35
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                         AAAAAAT 4689
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DEDNESS: both
            INVENTION:
                                                             Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
Mohr, Christine
Rebischung, Corinne
VENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
                                    Wendland, Jurgen
Knechtle, Philipp
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48.0%;
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Pred. No. 6.3e-05;
0; Mismatches 221;
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Best Local Similarity
Matches 310; Conserv
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TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
TYPE: nucleic acid
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 919-541-8587
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NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
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                                                                                                                                                                                                                                                                                              63
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REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
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Pred. No. 4.9e-05;
0; Mismatches 378;
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US-09-316-083-2
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APPLICANT: The Institute of Physical and Chemical
TITLE OF INVENTION: Endonuclease
FILE REFERENCE: pH-651
CURRENT APPLICATION NUMBER: US/09/316,083A
CURRENT FILING DATE: 1999-05-20
EARLIER APPLICATION NUMBER: JP98/141861
EARLIER FILING DATE: 1998-05-22
NUMBER OF SEC ID NOS: 38
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Best Local Similarity 51.68;
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TYPE: DNA
ORGANISM: Saccharomyces
FEATURE:
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Pred. No. 0.0001;
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RESULT 13

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; OTHER INFORMATION: /note- "RP4 origin of DNA transfer (oriT) from ; OTHER INFORMATION: plasmid RP4"
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Best Local Similarity
Matches 207; Conserv
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
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MEDIUM TYPE: Floppy disk
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3059 AAAGATTTAATTTTTTCAATTTTTAACAATACTTTTTGTAATATTATGTTTAAATTTAAATT 3118
                                                                                                                              2939 TCTTCATTTGTAATATTTAGATGATTTTACTAATTTTAGTTTTTATATATTAAATAATTAA 2998
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
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STREET: 1 South Pinckney Street
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Rood, Julian
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3770..4013
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Pred. No. 0.0001
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                                                              Query Match
Best Local Similarity
Matches 224; Conserv
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INFORMATION FOR SEQ ID NO:
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ORIGINAL SOURCE:
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APPLICATION NUMBER: CH 0
FILING DATE: 31-DEC-1996
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CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                        NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38
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                                                                                                                                                                   ORGANISM:
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Mohr, Christine
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Knechtle, Philipp
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/ENTION: GENOMIC DNA SEQUENCES
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                                                            Score 58.8; DB 4;
Pred. No. 0.00016;
0; Mismatches 237;
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TELEPHONE:
TELEFAX: 91:
INFORMATION FOR:
SEQUENCE CHARAC
                                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: CH 0016/97

FILING DATE: 31-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Me19s, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976

TELECOMMUNICATION INFORMATION:
TELEPHONE: 910-541-8587
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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ZIP: 27709
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5, 6239264
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   CHARACTERISTICS:
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7ENTION: GENOMIC DNA SEQUENCES OF
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STRANDEDNESS: Sira
TOPOLOGY: 1:
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Pred. No. 0.00016;
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Search completed: July Job time: 3987 sec 30, 2002, 11:11:03

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Maximum
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Perfect score:
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JOURNAL MEDLINE REFERENCE ACCESSION
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ORGANISM RESULT AF041051 LOCUS REFERENCE AUTHORS DEFINITION AUTHORS TITLE quaking aspen.

Populus tremuloides

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.

1 (bases 1 to 1172)

HLW.J. Kawaoka, A. Tsai, C.J., Lung, J., Osakabe, K., Ebinuma, H. and Chiang, V.L. promoter region. AF041051 AF041051.1 GI:3 Proc. Natl. 98226828 Compartmentalized expression of two structurally and functionally distinct 4-coumarate:CoA ligase genes in aspen (Populus 2 (bases 1 to 1172) Hu,W.-J. and Chiang,V.L. AF041051 1172 bp Populus tremuloides clone Pt4CLlp tremuloides) Kawaoka, A., Tsai, C.J., Lung, J., Osakabe, K., Ebinuma, H. and GI:3258638 Acad. Sci. U.S.A. 95 (9), 5407-5412 (1998) DNA linear PLN 26-JUN-1998 4-coummarate:CoA ligase gene,

Result No.

Score

Query Match Length DB

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Description

SUMMARIES

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Submitted (01-JUL-2001) Biology, Submitted (01-JUL-2001) Biology, Beijing Qinghua East Road No. 35,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Sosidae; eurosids I; Malpighiales; Salicaceae; Populus.
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Lu,H., |Zeng,Q. and Jiang,X.
Genomic DNA sequence of 4-coumarate:CoA ligase
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join(1153. 2136,3321. 3519,3644.
4174. 4284)
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1. .>1172
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MKGYLNDPEATSRTIDKEGWLHTGDIGYIDDDDELFIVDRLKELIKYKGFQVAPAELE
ALLIAHPEISDAAVVGLKDEDAGEVPVAFVVKSEKSQATEDEIKQYISKQVIFYKRIK
                                                                     AANPFSTPAELAKHAKASRAKLLITQACYYEKVKDFARESDVKVMCVDSAPDGCLHFS
ELTQADENEAPQVDISPDDVVALPYSSGTTGLPKGVMLTHKGLITSVAQQVDGDNPNL
YFHSEDVILCVLPMFHIYALMSIMLCGLRVGASILIMPKFEIGSLLGLIEKYKVSIAP
                                                      VVPPVMMSIAKSPDLDKHDLSSLRMIKSGGAPLGKELEDTVRAKFPQARLGQGYGMTE
                                                                                                                               /translation="mnPQEEFIFRSKLPDIYIPKNLPLHSYVLENLSNHSSKPCLING
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/protein_id="AAL02144.1"
/db_xref="GI:15636677"
                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                    join(1137.
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/db_xref="taxon:118781"
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Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota, Metazoa, Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
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Caenorhabditis elegans
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16; Conser
                                                                                                           Direct Submission
Submitted (05-OCT-2001) Department of University, Genome Sequencing Center,
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Sanger Centre, Hinxton Hall Cambridge CB10 IRQ, England email: rw@nematode.wustl.edu
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                                        Department of Genetics, Washington St. Louis , MO 63110, USA, and
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4444 Forest Park Avenue,
  jes@sanger.ac.uk
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neighboring submissions.
                                    NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between
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more than one m13 subclone. regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemist

NEIGHBORING COSMID INFORMATION

cosmid CELZK6 cosmid is Y39D8B;3' cosmid is Y39D8A. Actuals at base position 1 of CELZK6; actual end.
The orientation of this cosmid is unknown. DBA. Actual start of this actual end is at 40114 of

the Coding ing sequences below are predicted
program Genefinder(P. Green and)
 Location/Qualifiers ۲ from computer L. Hillier, ms in preparation). analysis, using

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FEATURES
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join(5937..60
7589..7687)
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3956. .4127,4306. .4441,4490. .4708)
/gene="ZK6.8"
/codon_start=1
/note-"similar to lysosomal acid lipases (SW:P38571); coded for by the following C. elegans cDNAs: yk263b10.3, yk263b10.5, yk30888.5, yk552a3.3, yk552a3.5, yk722d9.5, yk722d9.3, yk733a11.5, yk733g10.5, yk736f6.5, yk736f6.3, yk733g10.3, yk851d01.5"
                                                                                                                                                                                                                      DGWFDIFGAGEFLPNNWAMKLAAKDICGGLKVEADLCDNVLFLIAGPESDQWNQTRVP
VYATHDPAGTSTQNIVHWMQMVHHGGVPAYDWGTKTNKKKYGQSTTLPLSREPRFTST
GVMPIGWLIRLTCLTTY
                                                                                                                                                                                                                                                                                                                                   /product="Hypothetical protein ZK6.7b"
/protein_id="AALI1486.1"
/brotein_id="AALI1486.1"
/brotein_id="GI:15967144"
/translation="MMRFAVFLAAFFVQDVVGSHGDPELHMTTPQIIERWGYPAMIYT
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DAGFDVWLGNMRGNTYSMKHKDLKPSHSAFWDWSWDEMATYDLNAMINHVLEVTGQDS
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FVGCITFALLPSNDIGNCIESSKKIVAFRDGIALMYRAFRSPKMIVLIPTFVLTGVHT
SFWVSIYPTTLTENSHLSAMIYLPAIYSFGVGLGETTMGLLISFCSKRIKNFGMRPTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="Hypothetical
/protein_id="AAG45570.
/db_xref="GI:12019644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="coded for by the following
yk788c11.3, yk788c11.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Caenorhabditis
/strain="Bristol N2"
                                                                                                                                                                                                                                                                                                         VYYMGHSQGTLTMFSHLSKDDGSFAKKIKKFFALAPIGSVKHIKGFLSFFANYFSLEF
                                                                                                                                                                     join(5937. .6023,6070. .
7576. .7713,7765. .7881)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="ZK6.7"
/note="coded for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .6023,6070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nı protein ZK6.8"
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Mismatches

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Gaps

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Query Match
Best Local Similarity
Matches 16; Conserv
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100.0%; ilarity 100.0%; Conservative C
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join(9204: .934
10127: .10257:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12832..14865
/gene="ZK6.5"
join(12832..1
14731..14865)
                                                                                                           20442. .21787
/gene="ZK6.3"
join(20442. .20615,20667. .20801,21151.
                                                                                                                                                                                                                                                 AHREDLMANYHTSYLDPTIDEVIRINKVDYIRKSQSHQLNFYNWAFHCSLVTVDFMKK
FPFVNLLRFEDQKYLLKEFYIKLIVFISSKRSMSRGKECMTFPDGSDVLPPASSEWHI
SKISPNLENKIRCRLIGRLSELRITDEEYLLMCVLIFCNPSLSQLSENGRRLLTSYQH
                                                                                                                                                                                                                                                                                                                        /product="Hypothetical protein ZK6.4"
/protein_id="AA645579.1"
/db_xref="G1:12019653"
/translation="MVATNQKCAVCERFTTEFNYGVPSCNACKIFFRRLITRTTPVKK
/translation="MVATNQKCAVCERFTTEFNYGVPSCNACKIFFRLITRTTPVKK
CYLGENCFTKTPITQKCVFCRFQKCIOVGMTLPSYLHFGEQTEKCLLSTIONLMLLL
CYLGENCFTKTPITQKCVFCRFQKCIOVGMTLPSYLHFGEQTEKCLLSTIONLMLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(17012. .17074,17511. .17607,17658. .18272,18679. .18941)

//gene="zK6.4"

//note="contains similarity to C4-type zinc finger (Pfam;
zf-C4.hmm, score: 34.58) and to the ligand-binding domain
of nuclear hormone receptors (Pfam: hormone_rec.hmm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FSFVNLLRFEDOKNIMKEFYIKLTVLINSKQSMSCGKEGMTFPDGSDVLPPTSSEWGI
SKISQNLENKVRCRLIGRLSELRITDEEYLLINFKNFQKFSKILITFSSVFKAFYNFP
RTELSKIVSRKIEKHFQSTKILQIFPEVSSIFQKNLKFSTTFQNS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MLASNQTCAVCERFTTEFNYGVPSCNACKIFFRRLITRTAPVKQ
CYIGEHCFTKSPITKKCTFCRFQKCIQVGMTLPSYLHFGELTKEKCIDSTIQKLILME
AHRKDLMANYYTSYLNPTIDEVIRLNKVEYTRKSQNHQMSFYNWAFHCCLVTVDFMKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="Hypothetical protein ZK6.5"
/protein_id="AAG45580.1"
/db_xref="GI:12019654"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="contains similarity zf-C4.hmm, score: 37.95)"
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/gene="ZK6.5"
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ATVTPSHEQPLLFQPRRPSYSISDCNNRRNSLGSCFIFFLSPFLNLYHYVIGIPLLCV
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LNGVGFALYYTGNGGYITSHSTRQTIESNVSLSWSFGCCCMIVGSVIMAVITTVTQDQ
IPQLLDAVNVTIGGHGVERREGDGETYLLFSVFAAISSMAIFTFMLMPSQDVSNCIEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="Hypothetical
/protein_id="AAG45573.1
/db_xref="GI:12019647"
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VYATHDPAGTSTQNIVHWMQMVHHGGVPAYDWGTKTNKKKYGQANPPEYDFTAIKGTK
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VYYMGHSQGTLTMFSHLSKDDGSFAKKIKKFFALAPIGSVKHIKGFLSFFANYFSLEF
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VATDDGYILEMHRIPFGKTNVTWPNGKRPVVFMQHGLLCASSDWVVNLPDQSAGFLFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="Hypothetical protein ZK6.7a"
/protein_id="AAG45574.1"
/db_xref="GI:12019648"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               score: 38.56)"
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join(17012. .
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                                                                                                                                                                                           IKDGMDAAFCN"
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27: .10257,10841:
)1._.11716)
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                            Score 16;
Pred. No.
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341. .11029,11081. .11256,11314.
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                               1e+02;
                                                           DB 3;
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                                                        Length 40114;
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JOURNAL REFERENCE
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AUTHORS
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VERSION
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AC012256/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (21-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 18, 2001 this sequence version replaced gi:13357415. All repeats were identified using RepeatMasker: Smit, A:F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens chromosome 8, clone RP11-135G15 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (basés 1 to 173705)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG; HTGS_PHASE1; HTGS_DRAFT
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SEQUENCE, 18
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                                                                                                                                                                                                                                                               Sequencing vector: M13; M77815; 69% of reads sequencing vector: Plasmid; n/a; 31% of reads sequencing vector: Plasmid; n/a; 31% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 163867 bases at least Q30 Consensus quality: 168063 bases at least Q30 Consensus quality: 169817 bases at least Q20 Insert size: 172005; sum-of-contigs Quality coverage: 4.9 in Q20 bases; sum-of-contigs
                                           NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: L3739
Center clone name: 135_G_15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
1 1853: contig of 1853 bp in length 1854 1953: gap of 100 bp
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ne 8 clone RP11-135G15 map 8,
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WORKING DRAFT
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34390 40744: contig of 6355 bp
40745 40844: gap of 100 bp
40845 46688: contig of 5844 bp
46689 46788: gap of 100 bp
46689 55147: contig of 8359 bp
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107720 122838: contig of 15119 bp in length
122839 122938: gap of 100 bp
122939 136635: contig of 13697 bp in length
136636 136735: gap of 100 bp
136736 152397: contig of 15662 bp in length
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152498 173172; cont
173173 173272; gap of
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79479 93773: contig of 14295 bp in length
93774 93873: gap of 100 bp
93824 107619: contig of 13746 bp in length
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55248 65028: contig of 9781 bp in length
65029 65128: gap of 100 bp
65129 79378: contig of 14250 bp in length
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27167 30445: contig of 3279 bp in length
30446 30545: gap of 100 bp
30546 34289: contig of 3744 bp in length
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79479. 93773
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107720. .122838
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                         /note="assembly_fragment"
122939. .136635
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/db_xref="taxon:9606"
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/clone_lib="RPCI-11 Human Male
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3 173705: contig of
cocation/Qualifiers
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Mammalia; Eutheria; I
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16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (26-SEP-2001) Genetics, Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, Missouri 63108, USA Center project name: M_BA0285H09.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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                                                                            complete sequence. AL591003
                                                                                                      Mouse DNA sequence from clone
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a 32056 c 33141 g
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152498. .173172
/note="assembly_fragment"
173273. .173705
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40786 c 41518 g
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/db_xref="taxon:10090"
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Chordata;
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. 1.1e+02;
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 Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Mus
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-354124 is from the RPCI-23 Mouse PAC Library constructed by the group of Pleter de Jong.

For further details see http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                  SCYOL075C
S.cerevisiae chromosome
Z74817 Y13140
Z74817.1 GI:1419904
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                                                                                                                                                               Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
1 (bases 1 to 3545)
Direct Submission
Submitted (04-JUL-1996) Data
European yeast chromosome XV
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Location/Qualifiers
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                                                                                                               Unpublished
                                                                                                                                           Alexandraki, D., Katsoulou, C. and Tzermia, M.
                                                                                                                                                                                                                                                                       baker's yeast.
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50173. .50333
/note="Single clone region. Sequence from reads short insert library derived from a single pUC c Restriction digest data confirm the assembly." a 59303 c 59031 g 51255 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="13"
/clone="RP23-354124"
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Pred. No.
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XV reading
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collected by MIPS on behalf of the sequencing project. MIPS at the
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HOCkIng,D., Webb,E., Radcliff,F., Rothel,L., Taylor,S.,
Pinczower,G., Kapouleas,C., Braley,H., Lee,A. and Doidge,C.
Isolation of recombinant protective Helicobacter pylori antigens
Infect, Immun. 67 (9), 4713-4719 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oh 93.8%; Sil Similarity 100.0%; 15; Conservative 0;
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Hocking,D., Rothel,L., Do
Recombinant Helicobacter
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Helicobacter pylori
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                                     Hocking, D.,
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Martinsried, FRG: E-mail: Mewes@mips.embnet.org
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Submission
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APFFLAYMTLELPLSALASVLYAVFTVLACGLPRTAGNFFATVYCSFIVTCCGERLGI
MTNTFFERPGFVVNCISIILSIGTQMSGLMSLGNSRVLKGFNYLNPVGYTSMIIINFA
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HETKEILQSVRAIFKFGMINALMGPSGGSKSSLLNLISGRLKSSVFAKEDTSGSIMFN
DIQVSELMFKNYCSYVSQDDHLLAALTYKETLKYAAALTHHLTEAERMERTDNLI
SIGLKHCENNIIGNEFVKGISGGEKRRVTMGVQLLNDPPILLLDEPTSGLDSFTSATI
LEILEKLCREQGKTIITIHQPRSELFKFGNVLLAKSGRTARHGSDEMIAYFTEL
GYNCDSFTNVADFFLDLISVNYONGONEISSRARVEKILSAWKANNDNESLSPTPISE
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IMSIHOPRSDILFLLDQVCILSKGNVVYCDKMDNTIPYFBSIGYHYPQLVNPADYFID
LSSVDSRSDKEBAATGSFRUSLIDHNIDYERTHLDLQAEYISNATEIDIQNMTTRLD
FWKQVTVLTRRNFKLNFSDYVTLISTFAEPLIIGTVCGWIYYKDDKSSIGGLRTTTAC
LYASTILQCYLYLLFDTYRLCEQDIALYDRERAEGSVTPLAFIVARKISLFLSDDFAM
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TFTVLSMGCGFFVNAKVMPVYVRWIKYIAFTWYSFGTLMSSTFTNSYCTTDNLDECLG
NQILEVYGFPRNWITVPAVVLLCWSVGYFVVGAIILYLHKIDITLQNEVKSKQKKIKK
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/note="ORF YOL075c"
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/db_xref="taxon:4932"
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                             Rothel, L.,
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                             Doidge, C.,
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                         Radcliff, F.,
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LIWEKDTRSGEKNGIKDIKEQSIFIREIPLMTERTSFIINGVERVVNQLHRSPGVIF

KEEESSTSLNKLIYTGGIIPDRGSWLYEEYDSKDVLYARINKRRKVPVTILFRAMDYQ

KODIIKMEYPLLYWRYENDKYLIPFASLDANQRMEFDLKDPGKIILLAGKKLTSRKI

KELKENHLEWVEYPMDILINRHLAEPWWGKEYULDMLTQLDKNKLEKIHDLGVQEFV

IINDLALGHDASIIHSFLADYESLKILKQTEKIDDENALAAIRHKVMKPGDPVTTEV

AKQFVKKLFFDPERYDLTMVGRMKMHKLGLHVPDYITTLTHEDIITTVSKYLMKIN

QGKIDDRDHLGNRRIRAVGELLANELHSGLVKNQKTIKDKLTFNSGATDSLMPHDLVN

SKMITSTIMEFFMGGOLSQFMDQTNPLSEVTHKRKLSALGEGGLVKDRVGETILITAIQ

THYGRICPIDEGNIGLINTLSTFTRVNDLGFIEAPVKVVDGKVVGSTILITAIQ

EDSHIIAPASTPIDEEGNIGLISTLSEVTHKRRLSALGEGGLVKDRVGSTILITAIQ

FFLEHDDANRALMGTMMQRQAVPLLRSDAPIVGTGIEKIIARDSKGAIKANRAGYVEK

IDSKNIYILGEGKEBAYIDAYSLQKNLRTNQNTSFNOYPIXKYGDKVEAGQIIADGPS

MOCKEL NG CANNINASALMINGANAGANAGANAGANAGANAGANAGLIA
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786 c 1057 g 1185
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/product="pnA-directed RNA polymerase homolog"
/protein_id="AsA47279.1"
/db_xref="GI:1840152"
/translation="MSKKIPLKNRLRADFTKTPTDLEVPNLLLLQRDSYDSFLYSKDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to C. jejuni
and to E. coli DNA-directed
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VAGGAAAESEEKTEFNVILADSGAEKIKVIKVVREITGLGLKEAKDATEKTPHVLKEG
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/product="50S ribosomal
/protein_id="AAB47278.1"
/db_xref="GI:1840151"
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LAEEIKNGRIDFDMVIATPDMMAVVGKVGRILGPKGLMPNPKTGTVTMDIAKAVTNAK
SGGVNFRVDKKGNVHAPIGKASFPEEKIKENMLELVKTINRLKPSSAKGKYIRNAALS
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/protein_id="AAB47277.1"
/db_xref="GI:1840150"
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/strain="Hp921023"
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (17-MAR-1999) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peterson, S., Loftus, B., Richardson, D., Dodson, R., Khalak, H. Glodek, A., McKenney, K., Fitzegerald, L.M., Lee, N., Adams, M.D. Hickey, E.K., Berg, D.E., Gocayne, J.D., Utterback, T.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori 26695.
Helicobacter pylori 26695
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (06-AUG-1997) The Institute for Genomic Research, 9712 Medical Center D_{\Gamma}, Rockville, MD 20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 388 (6642), 539-547 (1997) 97394467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peterson, J.D., Kelley, J.M., Karp, P.D., Smith, H.O., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter,J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter
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b, J.-F., White, O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 17880)
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                                                                                                                                                                                                                                                                                                                                        /gene="HP1190"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1337. .2665)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(310. .1350)
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                                                                                                                                                                                                                                                       GB:X05345 GB:M96646 SP:P12081 32.39; identified by sequence
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LIFEAST LE RESUSE KENDEMINARIA EL PLIQUIARIANO I ENQUALISMILITAN LE LA PRETINEMINO EL L'EGTTKESRLIENIGALQVSWSQKELEIFQKELTAIKIEGARYPERINEMINO COMPLement (5626 . .5712)

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15; Conser
                                                                              Rattus norvegicus
Eukaryota; Metazoa;
Mammalia; Eutheria;
Muzny, D.M., Adams, C., Adio-Oduola, B.,
                                                                                                                                                                                                                                              AC107593
                                                                                                                                                                                                                                                                                                      Rattus
                                                          Rattus:
                                                                                                                                                                                           HTG; HTGS_PHASE1.
                                                                                                                                                                                                                    AC107593.1 GI:18266586
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                            (bases 1 to 26236)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                       norvegicus clone CH230-18605, unordered pieces.
                                                                                                                                                                     rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(8089. .8556)
/gene="HP1196"
/note="similar to SP:P22744 percent identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGAATMDWMEQEKERGITITSAATTCFWKDHQINLIDTPGHVDFTIEVERSMRVLDGA
VSVFCSVGGVQPQSETWWRQANKYGVPRIVTVWNMDRIGANFYXDYENQIKLRIKANPV
PINIFIGAEDTFIGVIDLYQMKAIVWNNETMGAKYDVEBIPSDLLEKAREVREKLVEA
VAEQDEALMEKYLGGEELSIEEIKKGIKAGCLNMSLVPMLCGSSFKNKGVQTLLDAVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="translation elongation factor EF-G (fusA)'/protein_id="AAD08239.1"
/db_xref="GI:2314354"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(8572. .8979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mkrkkapvrevlgdpvygnkvvtkfinkmmfdgkkgvaekiiyk
afnkieeksgekgievfekalervrplvevrsrrvggatyqvpvevrasrqqslsirw
ileatrkrnermmvorlanelmdaasdkgaafkkkedvhkmaeankafahyrw"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="ribosomal protein S7 (rps7)"
/protein_id="AAD08240.1"
/db_xref="GI:2314355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(8089. .8556)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       {\tt RRRGQINSMDDRLGLKIVNAFVPLVEMFGYSTDLRSATQGRGTYSMEFDHYGEVPSNI}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VFIKLEPKEPGSGYEFVNEISGGVIPKEYIPAVDKGIQEAMQNGVLAGYPVVDFKVTL
YDGSYHDVDSSEMAFKIAGSMAFKEASRAANPVLLEPMMKVEVEVPEEYMGDVIGDLN
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GGMGELHLEIIVDRLKREFKVEAEIGQPQVAFRETIRSSVSKEHKYAKQSGGRGQYGH
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LESGSYVYNSTKDKKERVGRLLKMHSNKREDIKEVYAGEICAFVGLKDTLTGDTLCDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="ribosomal protein S12 (rps12)"
/protein_id="AAD08241.1"
/db_xref="GI:2314356"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to SP:P18662 percent identity: identified by sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="HP1196"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MPTINQLIRKERKKVVKKTKSPALVECPQRRGVCTRVYTTTPKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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                                                                              Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 15;
Pred. No.
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                                                                                                                                                                                                                                                                                                                            26236 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                  DNA ______
5, *** SEQUENCING
Ali-osman, F.R., Allen, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 17880;
                                                                                                                                                                                                                                                                                                                            HTG 23-JAN-2002
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CDS

CDS gene

Davy Carroll, L. Dederich, D.A. Delaney, K. R. Delgado, O. Davy Carroll, L. Dederich, D.A. Delaney, K. R. Delgado, O. Denn, A.L. Ding, Y. Dinh, H.H. Douthwaite, K.J. Draper, H. Dugan-Rocha, S., Durbin, K.J. Earnhart, C. Edgar, D. Edwards, C.C., Elhaj, C. Escotto, M., Falls, T. Ferraguto, D. Flagg, N. Ford, J. Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hollins, B., Homsi, F., Howard, S., Hober, J., Hallyk, S., Hume, J., Jackson, L.E., Jaccbson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mouris, S., Moser, M., Nickeron, E., Nocheken, W., Suyen, N., Nickeron, E., Nockenkwo, S., Oguh, M., Okwuon, G., Oragunye, N., Oviedo, R., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruz, S., Savery, G., Scherer, S., Scott, G., Shan, H., Shooshtari, N., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, K., Thomas, S., Williams, G., Williamson, A., Wilstanon, A., Washington, C., Walliams, G., Williamson, A., Washington, C., Walliams, G., Williamson, A., Wester, R., Bon, D., Vinson, R., Wooden, S., Wooden, S., Walliams, G., Williamson, A., Wester, R., Bon, J., Reson, D., Weiston, R., Wooden, S., Walliamson, A., Williamson, A., Weiston, D., Weiston, Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Bhhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chon,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy,Carroll,L., Dederich,D.A., Delaney,K.R., Delagdo,O., Dathorne,S.R., David,R., Delagdo,O., Delaney,K.R., Delagdo,O., Delagdo,O., Delaney,K.R., Delagdo,O., Delaney,K.R., Delagdo,O., Delag Worley, K.C.
Direct Submission Unpublished 2 (bases 1 Direct Submission (bases 1 to 26236)

COMMENT

JOURNAL REFERENCE AUTHORS TITLE JOURNAL TITLE

Submitted (23-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Center: Baylor College of Medicine Center code: BCM

Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
Project Information

Center clone name: CH230-18605 Center project name: GOVS

findPhrapList Sequencing vector: Plasmid; M77789 Chemistry: Dye-terminator Big Dye: Chemistry: Dye-terminator Big Dye: 98% of reads Assembly program: Phrap; version 0.990329First call to

Consensus quality: 21752 bases at least Q40 Consensus quality: 23932 bases at least Q30 Consensus quality: 25882 bases at least Q20 Estimated insert size: 18630; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 0.1x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 17 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown

REFERENCE

SOURCE KEYWORDS VERSION ACCESSION

ORGANISM

DEFINITION LOCUS

AC107593 RESULT ф

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JOURNAL REFERENCE
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AC005942
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AUTHORS
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15; Conserv
                                                                                              AC005942
                                                                                                                                                                                                                                                                                                                Homo sapiens chromosome
                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                  human.
                                                                                                                                                                                                                                                                         AC005942.2
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/clone="CH230-18605"
4887 c 4901 g

    .26236
    /organism="Rattus norvegicus"

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Pred. No.
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of 1232
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AUTHORS
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JOURNAL
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                JOURNAL
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Submitted (06-JUN-2000) Whitehead Institute/MIT Center for Genome

Direct Submission

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Subramanian, A., Sun, C., Tesfaye, S., Torruella-Miller, I.,
Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, X., Wyman, D.,
Ye, W.J. and Zody, M.

Direct Submission

Sibmitted (13-0CT-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

Submitted (13-0CT-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

Submitted (13-0CT-1999) Whitehead Institute/MIT Center for Genome
Research, Jacobs Street, Cambridge, MA 02141, USA

Submitted (13-0CT-1999) Whitehead Institute/MIT Center for Genome
Research, J. Bardan, N., Backerly, R., Blen, J., Brown, M.,
Baker, J., Bardan, N., Beckerly, R., Benn, J., Brown, A.,
Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A.,
Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A.,
Castle, A., Cerny, J., Colangelo, M., Forrest, C.,
Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K.,
Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K.,
Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K.,
Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K.,
Cooke, P., Dearellano, K., Depayre, E., Devon, K., Dewar, K.,
Cooke, P., Devar, K., Depayre, E., Devon, K., Dewar, K.,
Cooke, P., Devar, K., Devar, K.,
Cooke, P., 
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Baker, J., Barna, N., Beckerly, R., Benn, J., Brown, A.,

Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A.,

Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A.,

Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A.,

Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K.,

Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C.,

Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G.,

Hagos, B., Heaford, A., Horton, L., Howland, J.C., Jones, C., Kann, L.,

Karatas, A., Lehozaky, J., Lieu, C., Locke, K., Macdonald, P.,

Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J.,

Meldrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J.,

Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B.,

Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P.,

Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A.,

Tesfaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A.,

Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrin, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Meldrin, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P., Skaletsky, H., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Sun, C., Tesfaye, S., Torruella, Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, X., Wyman, D., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, X., Wyman, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gage, D., Gardyna, S., Geraigery, K., Grant, G., Hagos, B., Heaford, A., Herena, L., Horton, L., Howland, J.C., Jacotot, L., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meldrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Nahf, R., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Torjander, N., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, Y., Wyman, D., Ye, W. J., Zhao, J. and Zody, M.
                                                                       Karatas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McBwan, P., McGurk, A., McBrann, K., McLaughlin, J., Meldrim, J., Molla, M., Morris, W., Morrow, J., Mychalecky, J., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy Skaletsky, H., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Sun, C., Tesfaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, X., Wyman, D., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, X., Wyman, D.,
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4 (bases 1 to 26458)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.
Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,
Castic,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,
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Vassiliev, H., Vo, A., Ye, W.J. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                                                                                                       Collymore,A., Cooke,P., Corliss,D., Depayre,E., Devon,K., Dewar,K., Donelan,L., Ferreira,P., FitzHugh,W., Forrest,C., Funke,R.,
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FEATURES
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All repeats were identified using RepeatMasker: Smit, A.F.A. Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://ftp.genome.washington.edu/RM/RepeatMasker.html
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4271. 4297
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                                                                                                                              complement (5230.
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complement(*^^*
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complement//'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="hCIT.298_B_15"
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._.3700
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HS212J10
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Matches 15; Conservative
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Submitted (05-7AN-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Dec 29, 1998 this sequence version replaced gi:4007136.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

IMPORTANT: This sequence is not the entire insert of clone 212J10.
                                                                                                                                                                                                                                                                                                                                                                      Human DNA sequence from clone 212J10 on chr
Contains ESTs and a GSS, complete sequence.
AL034401
                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                      HTG
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                                                                                                                                                                                                                                                                                                  Homo sapiens
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9152..9425
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/rpt_family="MER4-internal"
complement(6845. .7155)
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/rpt_family="AluSg/x"
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11961
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11092
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11425
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7156. .7355
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12180
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complement(8256. .8
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Pred. No. 4.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                          30208 bp DNA linear PRI 23-NOV-1999 clone 212J10 on chromosome Xq25-26.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence is 
feature key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The true left end of clone 448E20 (297196) is at 30109 in this sequence. The true right end of clone 417G15 (AL009174) is at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          It may be shorter because we only sequence overlapping once, or longer because we arrange for a small overlap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /www.sanger.ac.uk/HGP/ChrX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is from the library RPCII constructed at the Roswell Park Institute by the group of Pieter de Jong. For further see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="L2 repeat: matches 2551. .2745 of consensus"
complement(2474. .2892)
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/clone_lib="RPCI-1"
1166. .1275
                                                                                                                                                                                                                                                                                                           /note="L2 repeat: matches 2584.
12097. .12126
/note="10 copies 3 mer aac 100%
12662. .12972
/note="AluSq repeat: matches 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MER45 repeat: matches 1. 8860. .9149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="AluSx repeat: matches 1.
8688. .8859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Alux repeat: matches 2.
6908. 7088
                     /note="MSTB repeat: matches 1. 17435. .17491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/note="MIR repeat: matches 201.
                                                                   16805
                                                                                                              /note="MIR repeat: matches 20.
16380. .16697
                                                                                                                                                                                                  /note="MER5B repeat: matches 12.
14161. .14346
                                                                                                                                                                                                                                                 14015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="AluSx repeat: matches 32.
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                                                                                      'note="AluSq repeat: matches 1.
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                                                                                                                                                                                                                                                                      ca 87% conserved"
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Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Blinage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Brydnt, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Cyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Cyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Delgado, O., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Haylak, P., Hawes, A., Hollins, B., Homsi, F., Howard, S., Huber, J., Hube, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC099662.1 GI:16973712
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                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus
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ny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29510. .29650
/note="MIR repeat:
<2009 c 5771 g
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/note="MER5A repeat: matches 3.
18324. .18488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="AluJo repeat: matches 1.
26242. .26339
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25794. .26104
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19212. .19275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="41 copies 2 mer tt 76% conserved"
24307. .24617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note-"Alu repeat: matches 268.
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IN PROGRESS ***,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 40 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: plasmid; M77789

Sequencing vector: plasmid; M77789

Chemistry: Dye-terminator Big Dye: 99% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 19414 bases at least Q40

Consensus quality: 22250 bases at least Q30

Consensus quality: 24240 bases at least Q30

Consensus quality: 24040 bases at least Q30

Estimated insert size: 7952; sum-of-contigs estimation

Quality coverage: 0x in Q20 bases; sum-of-contigs estimation

Quality coverage: 0.1x in Q20 bases; sum-of-contigs estimation
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20581: gap of u
21432: contig c
21532: gap of u
22815: contig c
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of 891 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 1005 bp in length unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown length of 1313 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown length
of 1283 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of 1402 bp in length
unknown length
of 952 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of 1429 bp in length unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of 945 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown length
of 1282 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 860 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of 917 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown length
of 851 bp in l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of 266 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of 922 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of 936 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of 901 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of 897 bp in 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
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length
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AUTHORS
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AC110265
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Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C.,
Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M.,
McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T.,
Mlenga, V., Murphy, T., Naylor, J., Muyen, C., Nicol, R., Norbu, C.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, R., Seaman, J.,
Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Tonham, K., Trayers, M., Talamas, J., Tesfaye, S., Theodore, J.,
* NOTE: This record contains 79 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J. Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Vola, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S. Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (10-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 62490)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren, B., Linton, L., Nusbaum, C., Lander, E.,
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Mus musculus clone RP23-317B21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 62490)
                                                                                                                                                                                                                                                                                                                                                                Center project name: L22627
Center clone name: 317_B_21
                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Whitehead Institute/ MIT Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.8%; Score 15; DB 2; 100.0%; Pred. No. 4.3e+02
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LOW-PASS SEQUENCE SAMPLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 46363;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schupback, R., Seaman, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ali, A., Allen, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boukhgalter, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG 10-FEB-2002
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10976: contig of 706 i

11076: gap of 100 b

11767: contig of 601
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358: contig of 714 bp in

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14118: contig of 686
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            12: gap of 
28413: contig
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27612: contig of 713
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22784: contig of 683
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22001: contig of 676
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21225: contig of 684
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8: gap of 100 bp
6954: contig of 686 bp
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6676: gap of 100 bp
47363: contig of 687 bp
7463: gap of 100 bp
48161: contig of 698 bp
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076: gap of 100 bp
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Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N. P., Buhay, C.,
Burch, P., Burkett, C., Burrell, K. L., Byrd, N. C., Carron, T. F.,
Carter, M., Cavazos, S. R., Chacko, J., Chavez, D., Chen, G., Chen, R.,
Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C. D., Cox, C.,
Coyle, M. D., Dathorne, S. R., David, R., Davila, M. L., Davis, C.,
Davy-Carroll, L., Dederich, D. A., Delaney, K. R., Delgado, O.,
Denn, A. L., Ding, Y., Dinh, H. H., Douthwaite, K. J., Draper, H.,
Dugan-Rochas C., Dinh, H. H., Douthwaite, K. J., Draper, H.,
Dugan-Rochas C., Dinh, H. H., Douthwaite, K. J., Draper, H.,
Dugan-Rochas C., Dinh, H. H., Douthwaite, K. J., Draper, H.,
                                                                                                                                                                                                                                                                                                                                                    Submitted (23-OCT-2001) Human Genome Sequencing Center, Depaid of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:17062261.
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                                                                                                                                                                                                                         Center: Baylor College of Medicine Center code: BCM
Center project name: GFWG
Center clone name: CH230-103F13
----- Summary Statistics
                                                                                                                  Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 45 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
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Human immune syste	Human immune syste	HNRCR nucleotide s	DNA encoding novel	Human brain Expres	Pyrococcus abyssi	Pyrococcus abyssi	Drosophila melanog	Human liver associ	Human digestive sy	Human immune/haema		Human immune syste	Plasmid construct	Human immune syste	Human gene regulat	Human polynucleoti	First EcoR1 nucleo	Human polynucleoti	Human polynucleoti	Human polynucleoti	DNA encoding novel	DNA sequence of re	Human immune/haema	cDNA sequence #480	Human cDNA sequenc	Zea mays DNA fragm	Human heart O-fuco	Human immune/haema	Human Protease and	Human cDNA clone (Human breast cance	Human immune/haema	Human immune/haema	`	DNA encoding novel

ALIGNMENTS

RESULT AAX58644 12-NOV-1998; misc_feature misc_feature misc_feature Populus tremuloides. Aspen; 4-coumarate coenzyme A ligase; lignin; transgenic plant; tree; conifer; forestry; Pt4CL1; promoter; xylem; ss. Aspen 4-coumarate coenzyme A ligase Pt4CL1 gene promoter 16-AUG-1999 (first entry) AAX58644 standard; cDNA; 1172 BP. 20-MAY-1999. WO9924561-A2 98WO-US24138 /*tag= a /note= "box A, 914..924 /*tag= b /note= "box ! 1018..1033 Location/Qualifiers 888..893 /note= /*tag= "box P, ŗ cis-acting cis-acting element" cis-acting element" element"

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WPI; 1985-007981/02.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression exclusively in xylem tissue. It can be used to manipulate gene expression, and hence to engineer traits of interest, in the xylem tissue of target plants, e.g. to manipulation content or structure, or to enhance growth, cellulose content or other value-added wood qualities. Plants with all
                                                                 Shine J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA; 1440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16
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                                                                                                             AS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pBR289nif-2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 16; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by modulating 4-coumarate co-enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nitrogen-fixation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasmid pRt329nif-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    멂
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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RESULT 3

AAX13959;
XX AAX13959;
AC AAX13959;
XX 31-MAR-199
XX 31-MAR-199
XX GHPO prote
KW peptic ult
XX Peptic ult
XX Peptic ult
XX Helicobact
XX WO9843478
XX AL-Garawi
XX WPI; 1998
DR W
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUL-1997;
01-APR-1997;
24-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     When this gene is expressed in a Rhizobium sp., the bacterium produces useful products and plants may have their properties improved, e.g. the rate, quality and efficiency of the nitrogen-fixation process, especially in the root nodules of Rhizobium strains. See also AAN50526-7 and AAP50773-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GHPO protein;
peptic ulcer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H. pylori GHPO 741 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacterial strain contg. recombinant DNA Rhizobium strains for improved nitrogen
                                                                                                                                                                                                                                                                                                                                   Al-Garawi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9843478-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N
                                                                                                                                                                                    isolated Helicobacter polynucleotides - the diagnosis, prevention and treatment settions and gastrointestinal diseases
                                                                                                                                                                                                                                                                         1998-542293/46.
DB; AAW98240.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
15; Conser
                                                                                                                                                                                                                                                                                                                                                                            MERIEUX ORAVAX PASTEUR MERIEUX
                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN GENOME SCI INC
                                                                                                                                             Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fig 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease;
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                                                                                                                                                                                                                                                                                                                                   Kleanthous
                                                                                                                                               200-204;
                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0902615.
97US-0833457.
97US-0881227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US06371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 49..3030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16
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                                                                                                                                             2054pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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Pred.
                                                                                                                                                                                                                                                                                                                                   Miller C,
                                                                                                                                             English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gastroduodenal disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6; L
2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fixation
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of He
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                                                                                                                                                                                                                                                                                                                                      ₽P,
                                                                                                                                                                                                             Helicobacter
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                                                                                                                                                                                                                                                                                                                                   Tomb
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                                                                                                                                                                                                                               products
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these ulcer diseases.

ulcer diseases,

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gastric and duodenal

chronic, and atrophic gastritis, and duodenal ulcers. They can als

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 RESULT 4
AAS53676/c
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           The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the cc genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are CC pnemaoniae, Staphylococcus aureus, Salmonella typhi, Klebsiella CC pnemaoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets CC for antibiotic development. The antisense nucleic acids can also be used CC identify proteins used in proliferation, to express these proteins, CC and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in rational drug discovery CC programmes. The antisense nucleic acid sequence is also useful to screen CC programmes. The antisense nucleic acid sequence of cell proliferation in a wide varlety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation for the content of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1711 CTTTCACCAACCCCC 1697
                                                                                                                                                                                                                                                                                                                                      New polynucleotides antibiotics, compris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for the production of antibodies. detection and diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS53676
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                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haselbeck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2000;
23-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibiotic;
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15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ds; prokaryotic cellular pro
; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-191078P.
2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prokaryotic cellular proliferation
                                                                                                                                                                                                                                                                                                      No 7313;
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                                                                                                                                                                                                                                                                                                                                    for the identification and development se sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
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                                                                                                                                                                                                                                                                                                   511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zyskind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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patent did
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                                                                                                                                                                                                                                                       The invention relates to nucleic acid molecules from regions of the soybean genome which are associated with soybean cyst nematode (SCN) resistance. The nucleic acids are used to transform plants, and can produce soybean plants having an rhgl or an Rhg4 SCN resistant allele. The nucleic acids can be used for investigating rhgl or Rhg4 haplotypes of soybean plants and for introgressing SCN resistance or partial SCN resistance into cowhean allete.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Soybean; antihelmintic; gene therapy; soybean cyst nematode; SCN resistance; rhg1; Rhg4; SCN resistant allele; plant breec 240017 region G3; 318013 region A3; 515002 region G2; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the printed specification, format directly from WIPO at
                                                                                                                                                                resistance into soybean plants. They can also be used in plant breeding programmes. The invention also relates to proteins encoded by such nucleic acid molecules, as well as antibodies capable of recognising these proteins. The present sequence is a nucleic acid molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New purified nucleic acid for producing a soybean plant having soybean cyst nematode resistance and for use in plant breeding programs - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hauge
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                                                                                              Sequence 335913 BP; 114579 A;
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                            The invention relates to nucleic acid molecules from regions of the soybean genome, which are associated with soybean cyst nematode (SCN) resistance. The nucleic acids are used to transform plants, and can produce soybean plants having an rhg1 or an Rhg4 SCN resistant allel
           Human secreted protein-encoding
                                     17-JUL-2001
                                                              AAD05460;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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                                                                                      AAD05460 standard;
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                                                                                                                                                                                                                                                                   Sequence 335913
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             gene
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             22 cDNA clone HT4ES80,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a soybean plant having soybean plant breeding programs -
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s 0;
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amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 29 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, reaching a sthma, cognitive disorders, schizophrenia, asthma, asthma, cognitive disorders, schizophrenia, asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzhelmer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy;
                 gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding 29 human secreted polypeptides, preventing, diagnosing and/or treating e.g. cancers, Pdisease and diabetic retinopathy -
                                                                                                                          skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders,
                                                                                                                                                                                                                                                                                                                                                      The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the
                                                                                                                                                                                                                                                                                                                                                                                                                   AAD05389-AAD05473 represent cDNAs corresponding to 29 human secreted protein genes, and AAE01546-AAE01630 represent the proteins they encode. AAE01631-AAE01660 represent human secreted protein fragments or variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
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30-JUN-2000; 2000US-0215137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  foetal abnormality; developmental abnormality; haematopoietic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-316490/33
DB; AAE01617.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Komatsoulis GA,
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4..210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "Human secreted protein"
/transl_except= (pos:58..60, aa:Xaa)
/transl_except= (pos:178..180, aa:Xaa)
/note= "Xaa corresponds to any of the naturally occurring
L-amino acids; CDS does not include start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= c
/product= "Mature human secreted protein"
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tissues,
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Parkinson's
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RESULT
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AAI83975
                                                        The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human
         Note: The sequence data for this patent did not specification, but was obtained in electronic for at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                          diagnosing
                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2000;
18-MAY-2000;
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DB; AAO04044.
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15; Conserv
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2000US-0577409.
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                                                                                                                                                                                                                                         treating
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93.
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Pred. No. 3.9e
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No. 3
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11-JUL-2000

14-JUL-2000

26-JUL-2000

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14-AUG-2000

12-AUG-2000

22-AUG-2000

22-AUG-2000

22-AUG-2000

23-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; nootropic; neuroprotective; cytostatic; dermatological; viru immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulne antiparkinsonian; antistkling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparastic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccin
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11-JUL-2000;
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07-JUL-2000;
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28-JUN-2000;
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19-MAY-2000;
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17-MAR-2000;
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           2000US-0180628.
2000US-0186350.
2000US-0189874.
2000US-0198123.
2000US-020515.
2000US-02014886.
2000US-0211335.
2000US-0211486.
2000US-02114880.
2000US-0217487.
2000US-0217487.
2000US-0217487.
2000US-0217496.
2000US-0217496.
2000US-0217496.
2000US-02174518.
2000US-02252963.
2000US-0225267.
2000US-0225267.
2000US-02252775.
2000US-0225447.
2000US-0225475.
2000US-0225475.
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2000US-0225475.
2000US-02254681.
2000US-0225758.
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93.8%;
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06-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 11-SEP-2000

14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 30-AUG-2000; 01-SEP-2000; 01-SEP-2000; 01-SEP-2000; 01-SEP-2000; 05-SEP-2000; 05-SEP-2000; 06-SEP-2000;

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                                                                                                                                                    The invention relates to novel genes (ABA11004-ABA21534) and proteins CC (ABB14678-ABB18001) useful for preventing, treating or ameliorating comedical conditions e.g. by protein or gene therapy. The genes are comedical conditions e.g. by protein or gene therapy. The genes are comedicated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful comedicated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful comedicated from a range of human tissues and carriagonists are useful comedicated from ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (c) immune disorders e.g. Addison's disease, allergies, autoimmune constitutes, crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative coditis; (c) cardiovascular disorders such as myocardial ischaemias; (c) disease, multiple sclerosis, rheumatoid arthritis and ulcerative coditis; (c) cardiovascular disorders such as myocardial ischaemias; (c) disease; and (f) infectious diseases e.g. cerebral anoxia and come protein to the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                        Query Match
Best Local S
Matches 15
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17-NOV-2000
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06-DEC-2000
08-DEC-2000
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                                                                                                                             Sequence 457
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17-NOV-2000;
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DB; ABB14980.
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2000US-025391.
2000US-0251160.
2000US-0251030.
2000US-0251988.
2000US-0256719.
2000US-0251479.
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                                                                       Score 14.4; DB Pred. No. 4e+02;
                                                                                                                             86 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                    + Sequence Listing; English.
                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nervous system antigen polypeptides, and/or treating nervous system
                                                                                                                             144 T; 5 other;
                                                                                     22;
                                                        1:
                                                                                     Length
                                                          Indels
                                                        0;
                                                        Gaps
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2000US-022934 2000US-022934 2000US-022934 2000US-022934 2000US-022934 2000US-02295 2000US-023043 2000US-023124 2000US-023124 2000US-023124 2000US-023124 2000US-023196 2000US-023306 2000US-02330 2000US-02340 2000US-02340 2000US-02340 2000US-02340 2000US-02340 2000US-02340 2000US-02340 2000US-02340 2000US-023636 2000US-023636 2000US-023636 2000US-0241786 2000US-0241786 2000US-0241808 2000US-0241808 2000US-0241808 2000US-024647 2000US-024661 2000US-024652 2000US-024661 2000US-024661

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04-NOV-2000
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06-NOV-2000
08-NOV-2000

SEQ ID NO:25352

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RESULT 10
AAS64618/c
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                                       Ş
                                                                                                                                                                                                                                                 CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polyperase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC constant of the constant of
                                                                                                         Query Match
Best Local :
                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-2001; 2001WO-US08631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding novel human diagnostic protein #422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-FEB-2002 (first entry)
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                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 422; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drmanac RT, Liu C,
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532
                                                                                  Local Similarity 93.1
hes 15; Conservative
                                         1 cctttcaccaaccccc 16
                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
CCTTTCACCAATCCCC
                                                                                                                                                                                              606
                                                                                                                                                                                              B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          relates to isolated polynucleotide (I) and II) sequences. (I) is useful as hybridisation probes,
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93.8%;
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                                                                                                         Score 14.4; DB Pred. No. 4e+02;
                                                                                                                                                                                            133 G;
                                                                                     Mismatches
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RESULT

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AAK70540/c
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XX
AC AAK705
XX
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XX
Human;
XX
CS Homo S
XX
CS Homo S
XX
CYCost
XX

PR 09-AUG
PR 11-JAN
PR 16-MAI
PR 11-AUI
PR 11-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immune/haematopoietic antigen genomic sequence
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2000US-0229287.
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2000US-0224519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune/haematopoietic antigen; cancer;
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13-OCT-2000

13-OCT-2000

13-OCT-2000

20-OCT-2000

20-OCT-2000

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20-OCT-2000

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01-NOV-2000

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27-SEP-2000;
27-SEP-2000;
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21-SEP-2000;
21-SEP-2000;
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29-SEP-2000;
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25-SEP-2000;
2000US -0232398
2000US -0232400
2000US -0232401
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2000US -02334274
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2000US -0246527
2000US -0246611
2000US -0246611
2000US -0249211
2000US -
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic continuity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and currentment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased cc expression by rectifying mutations or deletions in a patient's genome ct that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting ct the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703 CC cancers and cancer metastases of haematopoietic antigen genomic conserved to present human immune/haematopoietic antigen genomic conserved to present invention. AAK64921 to AAK84950 and AAM82169 crepresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                     metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding useful for preventing,
Sequence 736 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
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2000US-0251479.
2000US-0251856.
2000US-0251868.
2000US-0251869.
2000US-0251989.
2000US-0251999.
2000US-0251997.
2000US-0254097.
                                                                                                                                                                                                                                                                                                                                                                   SEQ ID
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 125
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A; 218
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                                                                                                                                                                                                                                                                                                                                                                                                                      human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and
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 c;
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 192
 ç;
 201
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 Τ.
 0 other;
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QΥ
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                                Matches
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Best Local
571 CCTTTCCCCAACCCCC 556
        1 cctttcaccaaccccc 16
                              Similarity
15; Conserv
                                Conservative
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                              Score 14.4; DB 22;
Pred. No. 4.1e+02;
0; Mismatches 1;
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                                                736;
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RESULT 12
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AAK70541/c
ID AAK70541 standard; DN
XX
AC AAK70541;
XX
DT 06-NOV-2001 (first 6
XX
DT Human immune/haemator
XX
KW Human; immune; haemator
XX
KW Cytostatic; gene ther
XX
EV WO200157182-A2.
XX
PD WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-1 DNA; 736

(first entry)

Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25353.

cytostatic; gene therapy; vaccine; metastasis; Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

17-JAN-2001; 2001WO-US01354.

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31-JAN-2000
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01-NOV
 Nucleic
useful f
                                                 WPI;
                                                 2001-483426/52
                                                                               CA,
cids encoding human immune/hematopoietic for preventing, diagnosing and/or treating
                                                                                                                                           2000US-0236802
2000US-0237038
2000US-0237039
2000US-0239937
2000US-0241786
2000US-0241786
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2000US-02511930
2000US-02511930
2000US-02511939
2000US-02519399
2000US-02550978
                                                                                                               GENOME
                                                                                 SC,
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                                                                                 Ruben
                                                                                 SM;
   antigen polypeptides, cancers and
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RESULT 13
AAK70542/c
ID AAK70542:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 15
   31-JAN-2000

04-FEB-2000

24-FEB-2000

02-MAR-2000

16-MAR-2000

17-MAR-2000

18-AR-2000

19-MAY-2000

07-JUN-2000

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07-JUL-2000

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cytostatic; ge
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15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; DNA; 736
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2000US-018628
2000US-0184664
2000US-0188350
2000US-0189874
2000US-0199073
2000US-0199073
2000US-0209515
2000US-0219467
2000US-0214886
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2000US-021647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        haematopoietic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy;
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Pred. No. 4.1e+02;
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ine; metastasis; ds.
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
        amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703
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                                                                                                                                                                                                                                useful for metastasis
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17-NOV-2000;
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08-NOV-2000;
                                                                                                                                                                              AAK54951 to AAK64702 encode the human immune/haematopoietic antigen
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                                                                                                                                                                                                                                                          Nucleic
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2000US-0251988.
2000US-0251988.
2000US-0256719.
2000US-0256719.
2000US-0251479.
2000US-0251868.
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2000US-0251869.
2000US-0251869.
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2000US-0249300.
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                                                                                                                                                                                                                                           human immune/hemat diagnosing and/or
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                                                                                                                                                                                                                                                          immune/hematopoietic
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represent human

immune/haematopoietic antigen

genomic

ΩV 밁

cctttcaccaaccccc

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cctttccccaacccc

16 16 Query Ma Best Loc Matches

Local

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93

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Score 14.4; Depred. No. 4.1e 0; Mismatches

4.1e+02;

Indels Length

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Gaps

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22;

763;

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Match

cancers antigen

polypeptides, and

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Best Local
                                The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JAN-2000;
14-MAR-2000;
24-MAR-2000;
29-MAR-2000;
15-MAY-2000;
09-JUN-2000;
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Sequence
                                                                                                                                                                                                                                                                      Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                        Lillie
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                                                                                                                                                                                                                                                                                                                peptide useful as a
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15; Conserv
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763
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2000US-0189167.
2000US-0192099.
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2000US-0220534.
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178
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183
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other;
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RESULT 15
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AAH07529;
XX
AC AAH07529;
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AC AAH07529;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA clone (5'-primer) SI
XX
DE Human; primer; detection; diagr
XX
Cos Homo sapiens.
XX
Cos Homo sapiens
Cos Homo sapien
                                Query Match
Best Local
                                                                                                                                                                                                                                 sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH13633 represent human amino acid sequences; and AAH13620 to AAH13632 represent invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide comprises one of the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length chars defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length chars -
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15; Conservative
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Sugiyama T, Wakamatsu A, Nagai K,
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Copyright (c) 1993 - 2000 Comp
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ALIGNMENTS

SOURCE ORGANISM RESULT BB430167 LOCUS REFERENCE KEYWORDS VERSION ACCESSION DEFINITION TITLE JOURNAL AUTHORS Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Ishikawa, T., Kai, C., Kawai, J., Kikuchi, N., Izawa, M., Kagawa, H., Kojima, Y., Kondo, S., Kurihara, C., Kusakaba, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, Riken Mouse ESTS (Konno, H., et al.)
Unpublished (2000)
Contact: Yoshide Hayashizaki BB430167 218 bp mRNA linear EST 18-JUL-20 BB430167 RIKEN full-length enriched, adult male hippocampus Mus musculus cDNA clone C630031019 3' similar to X86406 R.norvegicus mRNA for brevican, GPI-anchored isoform, mRNA sequence. BB430167 Eukaryota; Mus musculus EST BB430167.1 GI:9269894 Mammalia; house mouse. mmalia; Eutheria; (bases 1 to 218) Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus EST 18-JUL-2000

COMMENT

Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222 Fax: 81-45-503-9216

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RESULT 2
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                           Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Köhn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R. Waterston, R. and Wilson, R. The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M.WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          445 bp mRNA linear EST (mq89g07,x1 Stratagene mouse heart (#937316) Mus musculus IMAGE:585948 3', mRNA sequence.
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Itoh.M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 445)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AI452374
AI452374.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / ADD_HOST SOUNA
/ ADD HOST SOUNA
/ ADD 
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/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hippocampus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="C630031019"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="RIKEN full-length enriched,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
Box 8501, St. Louis, MO 63108, USA
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Best Local S
Matches 16
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                                                                                                                                                                                   Contact: Robert B. We
University of Utah Ge
University of Utah
Rm. 308, Biomedical F
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16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
High quality sequence stop: 439.
Location/Qualifiers
                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Err
Plate: 0184 row: N COlumn: 2
                                                                                                                                  84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                       Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhaussern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ871533 564 bp DN
2M0184N21F Mouse 10kb plasmid UUGC1M
clone UUGC2M0184N21 F, DNA sequence.
              High quality sequence stop: 564
Location/Qualifiers
                                              Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                       Unpublished (2000)
                                                                                                                                                                                                                                                                                         Mouse whole genome scaffolding with paired end reads
                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 564)
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                                                                                                                                                                                                                                                                         plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="heart"
/dev_stage="13 day embryos"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus
/strain="NIH/Swiss"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:585948"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                       Genome Center
                                                                                                                                                                                                                                       Weiss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16; DB 9;
Pred. No. 2.4e+03;
Mismatches 0;
                                                                                                Std Error:
                                                                                                                                                                                                                                                                                                                                           Beacorn,T., Duval,B., Hamil,C.,
,M., Meenen,E., Pedersen,T., Reilly
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Brassica oleracea
Brassica oleracea
Brassica oleracea
Brassica; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                              Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001) Other_GSSs: BOGJO56TF
                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 796)
Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BH557406 796 bp
BOGJO56TR BOGJ Brassica oleracea
                                                                                                                                                                                                                                                                                                                                             Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BH557406.1 GI:17809186
                                                                                                                                                            Class: sheared ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143
                                                                                                                                                                                                    il: cdtown@tigr.org
is from a doubled haploid
                                                                                                                                                                                                                                              Medical Center Drive,
301-838-3523
301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance. **

123 c 103 g 195 t
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory Mouse DNA Resource
                     /db_xref="taxon:3712"
/clone="BOGJO56"
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/clone="UUGC2M0184N21"
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/strain="C57BL/6J"
                                                                  /organism="Brassica oleracea"
/strain="TO1000DH3"
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                                                                                                                             Location/Qualifiers
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Pred. No. 2.4e+03;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                              Rockville,
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                                                                                                                                                                                                                                                                                              20850, USA
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                                                                                                                                                                                                      Tom Osborn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SS
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В 5

165

RESULT 4 BH557406/c BASE COUNT ORIGIN

Query Match Best Local

Matches

REFERENCE AUTHORS TITLE

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678 CCTTTCACCAACCCCC 663
663 CCTTTCACCAACCCCC
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                                                                                   l Similarity
16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
http://image.llnl.gov
b column: 03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
BG771897
BG771897.1 GI:14082550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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602721709F1 NIH_MGC_97
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    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
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1 (bases 1 to 837)
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                                                                                                                                                                                                                                                                                                                             /note-"Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: Sall-XhOI (gtcgag); Oligo-dr primed using primer 5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched
                                                                                                                                                                                                                                       for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMM/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4838306"
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/lab_host="DH10B"
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Pred. No. 2.4e+03;
                                                                              Score 16; DB IV,
Pred. No. 2.4e+03;
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cDNA clone IM
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                                                1 (bases 1 to 190)
Zhao, S., Nierman, W., Feldblyum, T., Malek, J.,
B., Levins, M., Mcgann, S., Tsegaye, G., Geer,
                                                                                                                                                                                                                                                                        AZ299798
RPCI-23-439C15.TV RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Cameron, RA, Davidson, EH,
Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A sea urchin genome project: Sequence scan, virtual map, and additional resources '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 1024)
Cameron, R.A., Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R.,
Swartzell, S., Wallace, J.C., Poustka, A.J., Livingston, B.T., Wray
, G.A., Ettensohn, C.A., Lehrach, H., Britten, R.J, Davidson, E.H.
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                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                      Mus musculus
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Location/Qualifiers
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Fax: (626) 793-3047
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Unpublished (1999)
                    Mouse BAC End Sequences from
                                    and Fraser, C.M.
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                                                                                                                                                                                                                                                  DNA sequence.
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/clone="Plate=153 Col=21 Row=0"
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/db_xref="taxon:7668"
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                                                    Tsegaye, G., Geer, K., Krol, M.,
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JOURNAL
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                                                             Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea Ch Genetics (lifo@resgen.com). BAC end page: http://www.tigr.org/rdb/bac_ends/mouse/bac_end_intro.html Plate: 439 row: C column: 15
Clones are derived from the mouse BAC library RPCI-23. For library availability, please contact Pieter de Jong
                                                                                                                                                                                          Mouse BAC End Sequences from Library RPCI-23 Unpublished (1999)
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Other_GSSs: RPCI-23-439C15.TJ Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 246)
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В.,
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                                         szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     szhao@tigr.org
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-439C15"
/clone_11b="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI wethylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
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                                                                                                                                                                                                                                                          Geer,K.,
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                                                                                                                                                                                                                                                            Krol, M.,
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AA503034/c
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                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov

Tissue Procurement: David G. Bostwick, M.D., Rodrigo F. Chuaqui,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA503034 329 bp mRNA linear EST 19-AUG-199 nh58b03.s1 NCI_CGAP_Pr8 Homo sapiens cDNA clone IMAGE:956525 similar to gb:D10667 MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (HUMAN);contains element PTR7 repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 294 row: J column: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 329)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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/db_xref="taxon:10090"
/clone="RPCI-23-294J24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .246
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                                                                          /clone="IMAGE:956525"
                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="RPCI-23"
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/tissue_type="prostate"
                                               /clone_lib="NCI_CGAP_Pr8"
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1 (bases 1 to 353)

Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K. Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.

Use of BAC End Sequences for Sequence-Ready Map Building (1998) Other_GSSs: RPCI11-17C17.TV
                                                                                                                                                                                                                                                                                                                                                                                                          Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS.
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RPCI11-17C17.TP RPCI-11 Homo
                                                                                                                                                                                                                                                                                                                                                             Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B82624.1
                                                                                                                                                                                                                                                                                                                                                                                             http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9712 Medical Center Dr., Rockville, MD 20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pAMP10; mRNA made from invasive prostate
tumor, cDNA made by oligo-dT priming. Non-directional:
cloned. Size-selected on agarose gel, average insert
size 600 bp. "
                                                                                                                                          /note="Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI;
RPCII1 Human Male BAC Library"
60 c 65 g 126 t
                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="RPCI-11-17C17"
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                                                                                                                                                                                                                   /sex≈"Male"
                                                                                                                                                                                                                                    /clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="GDB:7506208"
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                                                                                                                                                                                                /cell_type="Lymphocytes"
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Pred. No. 6.5e+0
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clone RPCI-11-17C17,
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                                                                                                                                                                                              CCTTTCACCAACCCC 367
                                       AV212743 AV212743 RIKEN full-length enriched, ES cells Mus musculus cDNA clone 2410118E09 3' similar to D85818 Mouse mRNA for RNA polymerase
                                                                                                                                                                                                                                                                                15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dias Néto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstéin,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IL2-CS0048-221100-249-D11 CS0048 Homo sapiens cDNA, BF766646
    II subuunit RPB14, mRNA sequence
AV212743
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221100-249-D11&t3=2000-11-22&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: colon_est; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                                                                                                                                                                                                                                                                                    tissue mRNA and cDNA amplification
low stringency conditions."
101 c 62 g 112 t
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/clone_lib="CS0048"
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The Institute of Physical and Chemical Research (RIKEN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
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URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
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Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Yoshihide Hayashizaki
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                                 prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
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/clone="2410118E09"
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/strain="C57BL/6J"
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/lab_host="SOLR"
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509959 MARC 3BOV Bos taurus
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sequence.
                                                                                                                                                                                                                                             l Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
v0.980904.e. vector identified by cross_match with the -minscore 18
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Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, UTTel: 402 762 4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett Gasas,E., Wray,D.E., Legreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Cet
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BM106270.1 GI:17037340 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plate: 103 row: 0 column: 12
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus
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                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fet. longissimus muscle."

94 c 102 g 118 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Bos taurus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="pooled"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                 425 bp mRNA linear NCI_CGAP_Brn25 Homo sapiens cDNA clone IN contains TAR1.tl TAR1 repetitive element
                                                                                                                                                                                                                                                             93.8%; Score 15; 100.0%; Pred. No.
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IMAGE:2499846 3'
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Matches 15
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                                                  AUTHORS
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CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sc Clone distribution: NCI-CGAP clone distribution in found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 822 Std Error: 0.00
                                                                                                                                                                                                 AQ880479 507 bp DNA linear GSS 09-NOV-
HS_5044_A2_G02_SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=8812 Col=4 Row=M, DNA sequence.
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15; Conserv
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Seq primer: -40UP from Gibco
High quality sequence stop: 416.
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1 (bases 1 to 425)

1 (bases 1 to 425)

NCI/WINDS-CGAP http://www.ncbi.nlm.nih.gov/nclcgap.

NATIONAL Cancer Institute / National Institute of Neurological
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EST.
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Tissue Procurement: David N. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                 Mahairas, G.G., Wallace
Keller, A., Shaker, R.,
                                                                                                                   Homo sapiens
Sequence-tagged connectors: A sequence approach to mapping and
                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                      numan
                                                              (bases 1 to 507)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:2499846"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Metazoa;
                                                                                                                                                                     GI:6311946
                                                                                                                                                                                                                                                                                                                                                                                                     93.8%;
                             Wallace,J.C., Smith,K., Swartzell,S., ker,R., Furlong,J., Young,J., Zhao,S.,
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Primates;
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ches 0;
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                                                                                   Hominidae;
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                                 Holzman,T.,
Adams,M.D.
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ORIGIN
Search completed: July 29, 2002, 23:22:40 Job time: 6816 sec
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                                                                                                                                                                                                   Query Match 93.8%; S
Best Local Similarity 100.0%;
Matches 15; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                           Contacti Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3618
Fax: (206) 616-3687
Email: jwallace@u washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 8812 row: M column: 4
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Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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Location/Qualifiers
1. .507
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                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

141 a 117 c 107 g 135 t 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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/clone="plate=8812 CoL=4 Row=M"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="male"
                                                                                                                                                                                                     Score 15; DB ; Pred. No. 6.5; 0; Mismatches
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6.5e+03;
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Title:
Perfect score:
Sequence:

US-09-530-663B-15 16 1 cctttcaccaacccc

cctttcaccaacccc

Scoring table:

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Copyright (c) 1993 - 2000 Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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Sequence 16, Appli Sequence 4, Appli Sequence 7, Appli Sequence 4, Appli Sequence 6, Appli Sequence 8, Appli Sequence 5, Appli
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US-08-978-741-16
; Sequence 16, Application Us;
; Patent No. 6100076
; GENERAL INFORMATION:
; TOANT YANG Wang,
                                                                                                                         ; SEQUENCE CHARACTERISTICS:
; LENGTH: 1100 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-978-741-16
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    Вþ
                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P104
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/252-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ. ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0000
                                                         Query Match
Best Local Similarity
Matches 15; Conserv
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FILING DATE: 26-NO. 6100076-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/792498
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Yang Wang
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
    166
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CITY: South San Francisco
STATE: California
COUNTRY: USA
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US-08-975-762-40
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US-09-106-582-40
US-09-106-582-40
US-08-940-332-1
US-08-94-078-3
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US-09-362-831-10
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                                                                      Score 14.4;
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2: /cgn2_6/ptodata/2,

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4: /cgn2_6/ptodata/2,

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6: /cgn2_6/ptodata/2,

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB Maximum DB Total number Searched:

seq

length:

0;

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; SEQ ID NO 16
; LENGTH: 1100
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-333-729A-16
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US-08-978-741-4
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APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-Fucosyltransferase
FILE REFERENCE: P1041P1D1 - Substitute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/333,729A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: US 08/798,741
PRIOR FILING DATE: 1997-11-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compation operating SYSTEM: PC-DO SOFTWARE: WinPatin (Generation Data:
                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: 3.5 inch, 1.44 mb floppy
COMPUTER: LBM PC compatible
                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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TITLE OF INVENTION: O-Fucosyltransferase
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                                                                                                                                                                                                                                                                                                FILING DATE: 26
CLASSIFICATION:
                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/978,741 FILING DATE: 26-No. 6100076-1997 CLASSIFICATION: 435
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                  TOPOLOGY:
                                                                 LENGTH:
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Nucleic Acid
SEDNESS: Single
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California
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1 DNA Way
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Pred. No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/33,729A CURRENT FILING DATE: 1999-06-15 PRIOR APPLICATION NUMBER: US 08/798,741 PRIOR FILING DATE: 1997-11-26 NUMBER OF SEQ ID NOS: 21 SEQ ID NO 6 SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08978741 Patent No. 6100076 GENERAL INFORMATION:
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Best Local Similarity
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Best Local Similarity
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APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-Fucosyltransferase
FILE REFERENCE: P1041P1D1-Substitute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
          FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
NAME: SVOBODA, Craig G.
                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Yang Wang, Michael W. Spellman
TITLE OF INVENTION: O-Fucosyltransferase
NUMBER OF SEQUENCES: 17
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                                                                                                                       APPLICATION NUMBER: US/08/978,741 FILING DATE: 26-No. 6100076-1997
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                                                       APPLICATION NUMBER: FILING DATE: 31
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 REGISTRATION NUMBER:
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39,044
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Pred. No. 52
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Pred. No. 52;
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GENERAL INFORMATION:
APPLICANT: Wang Yang
APPLICANT: Well yang, Michael W.
TITLE OF INVENTION: O-FUCOSYltransferase
FILE REFERENCE: P1041P1D1-Substitute
CURRENT APPLICATION NUMBER: US/09/333,729A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: US 08/798,741
PRIOR APPLICATION NUMBER: US 08/798,741
PRIOR FILING DATE: 1997-11-26
NUMBER OF SEG ID NOS: 21
SEG ID NO 2
SEG ID NO 2
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US-08-978-741-7
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            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
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                                                                                                                                                                                APPLICANT: Yang Wang, Michael W. Spellman TITLE OF INVENTION: O-Fucosyltransferase NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                  NERAL INFORMATION: APPLICANT: Yang W
CURRENT APPLICATION DATA:
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166 CCTTTCACCAACCTCC 181
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Local Similarity 93.8%;
nes 15; Conservation
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TOPOLOGY: Linear
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                                                                                                     COUNTRY:
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                                                                                                                                                                    ADDRESSEE:
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San Francisco
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Pred. No. 53;
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; NUMBER OF SEQ ID NOS: ;
SEQ ID NO 8
; LENGTH: 5009
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-333-729A-8
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                                                                                                                                                                RESULT
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                                                                                                                      Sequence 5, Application US/08978741 Patent No. 6100076
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Best Local Similarity
Matches 15; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, Yang
APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-Fucosyltransferase
FILE REFERENCE: P1041P1D1-Substitute
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 5009 base pairs
TYPE: Nucleic Acid
                                                                                                    GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                          NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
ADDRESSEE: Genentec
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PRIOR APPLICATION NUMBER: (
                                                                     APPLICANT: Yang Wang, Michael W. Spellman
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STREET:
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Pred. No. 6:
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Pred. No. 61;
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COUNTRY: USA

94080

1.44 Mb floppy disk

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; LOCATION: 1..79
US-08-463-903-78
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                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                       SOFTWARE: MS-Word for Windows, Ver. 7.0
SEQ ID NO 78
LENGTH: 79
                                                         Matches
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APPLICANT: Mezes, Peter S.
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Best Local :
                                                                                                                                                                                                                                                                                                       APPLICANT: Richard, Ruth A.
APPLICANT: Richard, Ruth A.
APPLICANT: Kotite, Voseph A.
APPLICANT: Dimer and Multimer Forms of Single Chain Polypeptides
FILE REFERENCE: 40224A US
CURRENT APPLICATION NUMBER: US/08/463,903
CURRENT FILING DATE: 1995-06-05
EARLIER APPLICATION NUMBER: US 07/935,695
EARLIER APPLICATION NUMBER: US 07/935,695
EARLIER FILING DATE: 1992-08-21
NUMBER OF SEQ ID NOS: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/792498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb |
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
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TYPE: Nucleic Acid
STRANDEDNESS: Single
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ctttcaccajacccc 15
                                                     14;
                                                 87.5%; Score 14; DB ilarity 100.0%; Pred. No. 61 Conservative 0; Mismatches
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Pred. No. 66;
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61;
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; NAME/KEY: Drb-3AHV3' primer; LOCATION: 1..95
US-08-463-903-79
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; NAME/KEY: DRb-3AH5' primer
; LOCATION: 1..79
; OTHER INFORMATION: :
US-07-935-695-78
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SEQ ID NO 78
LENGTH: 79
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Patent No.
                      Query Match
Best Local Similarity
                                                                                                                                                                                                                            SEQ ID NO 79
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Best Local Similarity
Matches 14; Conserv
     Matches
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APPLICANT: Kotite, Nicolas J.
TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
FILE REFERENCE: 40224A US
CURRENT APPLICATION NUMBER: US/07/935,695
CURRENT FILING DATE: 1992-08-21
PRIOR APPLICATION NUMBER: US 08/463,903
PRIOR APPLICATION NUMBER: US 08/463,903
PRIOR FILING DATE: 1995-06-05
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                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/08/463,903
CURRENT FILING DATE: 1995-06-05
EARLIER APPLICATION NUMBER: US 07/935,695
EARLIER FILING DATE: 1992-08-21
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Mezes, Peter S.
APPLICANT: Richard, Ruth A.
APPLICANT: Affholter, Joseph A.
APPLICANT: Kotite, Nicolas J.
TITLE OF INVENTION: Dimer and Multimer Forms
FILE REFERENCE: 40224A US
                                                                                                                                                                                                                                         SOFTWARE: MS-Word for Windows, Ver. 7.0
                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 102
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                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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o. 6071515
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     Conservative
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                   87.5%; Score 14;
100.0%; Pred. No.
     0;
     Mismatches
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                      DB 3;
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                                                                                                                                                                                                                                                                                                                                                                   of Single Chain Polypeptides
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                                    Length 95;
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Gaps
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Query Match
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US-07-935-695-79
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US-08-485-657A-4
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SEQ ID NO 79
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CURRENT APPLICATION NUMBER: US/07/935,695
CURRENT FILING DATE: 1992-08-21
PRIOR APPLICATION NUMBER: US 08/463,903
PRIOR FILING DATE: 1995-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kotite, Nicolas J. TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides FILE REFERENCE: 40224A US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mezes, Peter S. APPLICANT: Richard, Ruth P. APPLICANT: Affholter, Jose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPUTED: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
CORRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                            STREET: 300
CITY: Chicago
CITY: Illinois
TELECOMMUNICATION INFORMATION: TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kirschling, Deborah J
APPLICANT: Gudkov, Andrei
APPLICANT: Roninson, Igor B
                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Roninson, Igor B
TITLE OF INVENTION: Genes and Genetic Elements Associated
TITLE OF INVENTION: with Sensitivity to Cisplatin
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                  NAME: NO. 5942389nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-N
                                                                                                           FILING DATE: 07
CLASSIFICATION:
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                                                                                                                                              APPLICATION NUMBER: US/08/485,657A
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Affholter, Joseph A.
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100.0%;
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Pred. No.
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                                                                                                                                                                                    Version
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Search completed: July 29, Job time: 4754 sec
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Best Local S
Matches 14
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                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PI
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                                                                                                                                                                                                        LENGTH: 208 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: GENTITLE OF INVENTION: with NUMBER OF SEQUENCES: 21 COMPUTER READABLE FORM:
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LENGTH: 206 base pairs
                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
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14; Conserv
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                                                                                                                          Conservative
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                                                                                                                                       83.8%;
93.3%;
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93.3%;
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Pred. No. 1.4e+02;
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Pred. No. 1.4e+02;
0; Mismatches 1;
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Method for HLA Typing
Patent: US 5545526-A 16 13-AUG-1996;
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Apple,R.J., Erlich,H.A., Griffith,R.L. and Schamethods and reagents for HLA DRDeta DNA typing Patent: US 5567809-A 77 22-OCT-1996;
Location/Qualifiers
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Apple, R.J., Erlich, H.A.,
Methods and reagents for
Patent: US 5567809-A 168
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1 (bases 1 to 19)

Apple, R.J., Erlich, H.A., Griffith, R.L. and Scharf, S.J. Methods and reagents for HLA DRDeta DNA typing Patent: US 5567809-A 191 22-OCT-1996; Location/Qualifiers
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Apple,R.J., Erlich,H.A., Griffith,R.L. and Scharf,S.
Methods and reagents for HLA DRbeta DNA typing
Patent: US 5567809-A 223 22-OCT-1996;
Location/Qualifiers
                                    1 (bases 1 to 24)
Whittaker, J.L. and Morten, J.E.
HUMAN MHC CLASS II DOUBLE TRANSGENE
Patent: WO 9503331-A 9 02-FEB-1995;
ZENECA LTD (GB)
           Other publication AU 7231494
Other publication GB 2280186
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Sheppard, P.O., Piddington, C.S. and Ellsworth, J.L.
Testis specific glycoprotein zpep10
Patent: US 6242588-A 10 05-JUN-2001;
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Sequence 9 from Patent W00066748.
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AX044055.1 GI:11342933
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artificial sequence.
1 (bases 1 to 39)
Hawkes,T.R., Warner,S.A., Andrews,C.J.,
Pickerill,A.P.
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Sequence 9 from Patent WO0066747
AX044109 AX044109.1 GI:11342987
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Patent: WO 0066747-A 9 09-NOV-2000;
ZENECA LIMITED (GB)
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1 (Dases 1 to 39)

Hawkes,T.R., Warner,S.A., Andrews,C.J.,
pickerill,A.P.
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Patent: WO 0066748-A 9 09-NOV-2000;
ZENECA LIMITED (GB)
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                           Sequence 76
AR097013
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Stinchcomb,D.T. and McSwiggen,J.A.
Interleukin-2 receptor gamma-chain ribozymes
Patent: US 5807743-A 1354 15-SEP-1998;
                                                                                                                                                                                                                                                                                           Unknown
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Sequence 1354 from patent
AR040506
AR040506.1 GI:5959869
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Hawkes, T.R., Warner, S.A., Andrews, C.J., Bachoo, S. and
Pickerill, A.P.
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Sequence 9 from Patent W00066746
AX044157
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Patent: WO 0066746-A 9 09-NOV-2000;
ZENECA LIMITED (GB)
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/db_xref="taxon:32630"
/note="Primer"
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Akaqi, H., Fujimura, T., Yokozeki, S. and Inagaki, A.
MICROSATELITE MARKER FOR DISCRIMINATING RICE PLANT CULTIVAR
TEST FOR PURITY OF PLANT SEED
Patent: JP 1998057073-A 28 03-MAR-1998;
MITSUI PETROCHEM IND LTD
OS OTYZA SATIVA
PN JP 1998057073-A/28
PD 03-MAR-1998
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Sequence
AR097014
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Mezes, P.S., Richard, R.A., Affholter, J.A.
Dimer and multimer forms of single chain
Patent: US 6071515-A 77 06-JUN-2000;
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Mezes, P.S., Richard, R.A., Affholter, J.A.
Dimer and multimer forms of single chain
Patent: US 6071515-A 76 06-JUN-2000;
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25 c 17 g
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16 c 24 g
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Pred. No. 4.1e+04;
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41 TCTCACCAACC 31
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PR 13-JUN-1996 JP 96P 152657
PI AKAGI HIROMORI, FUJIMURA TATSUTO, YOKOZEKI SUKEYOSHI, PI INAGAKI AKIKO
PC CIZN15/09,C12Q1/68;
CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
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FT repeat_region 1..131
FT repeat_region 1..131
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/organism='Oryza sativa'
T repeat_region 1..131
/pt_family='microsatellite'.
Location/Qualifiers
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/organism="Cryza sativa"
/db_xref="taxon:4530"
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tctcaccaacc 11
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	ABI.30817	AAQ26251	ABL31303	AAQ26196	AAQ26124	AAF92638	AAV16578	AAT41819	AAX79382	ID	
	Human HLA genotypi	HLA-DR beta sub-ty	Human HLA genotypi	HLA-DR beta sub-ty	HLA-DR beta sub-ty	HLA-DR typing prob	Probe G86 used to	HLA allele, HLA-DR	HLA-DR typing prob	Description	

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284 135 269 269 358 366 486	351 587 114 459 582	615 125 729 980 930	364 364 375 374 390 1562	7746 7757 7757 7757 7757 7757 7757 7757
Arabidopsis DR1. Synth HLA allele DRB1*1105 a DRB1*1305 a HLA-DR beta	Human naematolo Spleen necrosis Eucaryotic gene HLA-DR beta alli		Mouse alpha-1, Rice EPSPS PCR Primer G1. Sy Primer G1. Sy Primer G1. Sy Canine II-2 re Human secreted Microsatellite	Glucanase genomi Human HLA genoty Human HLA genoty Oligonucleotide HLA-DR beta sub- HLA-DR typing pr Probe VALB6 usec HLA-DR typing PCR Gene typing PCR Oligonucleotide Human testis spe
is the al al	naematologic necrosis vi otic gene ex beta allele beta allele	t beta allele secreted pro foetal liver brain expres bone marrow #19586 used	alpha-1,3 ga alpha-1,3 ga psps PCR pri G1. Synthe G1. Synthe II2 recept secreted pro atellite mar	Glucanase genomic Human HLA genotypi Oligonucleotide pr HLA-DR beta sub-ty HLA-DR typing prob Probe VAL86 used t HLA-DR typing prob Gene typing PCR pr Oligonucleotide pr Oligonucleotide pr Oligonucleotide pr Oligonucleotide pr

ALIGNMENTS

RESULT 1
AAX79382/c
ID AAX793
XX AAX793
XX 17-AUG
AC AAX793
XX Tissue
KW Tissue
KW major
KW major
KW sequen
XX Synthe
XX US5468
XX US5468
XX 27-JUN
PR 08-APF
XX 71-SUN
PR 08-APF
XX 727-JUN
PR 08-APF
XX 74-SUN
PR 08-APF
XX 75-SUN
PR 08-APF
XX 75-S 17-AUG-1999 AAX79382; AAX79382 standard; DNA; 12 BP. (first entry)

Tissue typing; human leukocyte antigen; HLA: MHC; donor; allele; PCR; major histocompatibility complex; bone marrow transplant; primer; amplification; polymerase chain reaction; probe; polymorphism; sequence-specific oligonucleotide probe hybridisation; ss.

HLA-DR typing probe G86.

Synthetic.

US5468611-A.

21-NOV-1995

08-APR-1993; 93US-0045530

27-JUN-1990; 08-APR-1993;

90US-0544218. 93US-0045530.

(BLOO-) BLOOD CENT RES FOUND INC

Baxter-Lowe LA, Gorski JA;

WPI; 1996-010091/01.

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RESULT
AAT41819
ID AAT4
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Best Local S
Matches 11
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The sequences given in AAT41811-20 represent probes which were used to resolve the human leukocyte antigen (HLA) DRB1 atleles, DRB1*08, *12 and *1404. This probe sequence hybridises to the Gly86 coding region found in alleles *0801, *0802, *0803 and 0805. These probes may be used in the method of invention which concerns HLA typing of a sample for an unknown pair of alleles. The pair of alleles comprises one of two known types which have the same overall set of polymorphisms but have a different distribution of polymorphisms between their two alleles. The
                                                                                                                                                                                Human leukocyte antigen typing of tissue samples - using allele-specific amplification to distinguish allele pair
                                                                                                                                                                                                                                                                                                                                01-MAR-1993;
27-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                               13-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                               US5545526-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human leukocyte antigen; HLA; allele; HLA-DR*08; HLA-DR*12; polymorphism; amplify; conserved region; detection; primer; tissue matching; identifying disease susceptibility; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT41819 standard; DNA; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12 BP; 2 A; 0 C; 7 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A novel method of typing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Column 19-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Improved method for HLA typing - by DNA amplification and sequence-specific oligo:nucleotide hybridisation, used to select bone marrow donors
                                                                                                                                                  Example
                                                                                                                                                                                                                                                                                                                                                                               27-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLA allele,
                                                                                                                                                                                                                                                                                                (BL00-)
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                                                                                                                                                1; Column 19; 24pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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90US-0544218.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the human leukocyte antigen (HLA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
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Pred. No.
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                                                                                                                                                                              distinguish allele pairs
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Probes AAV16561-624 are used to identify differences in the DR region human major histocompatibility complex (HLA-DR). The specification describes a method for HLA-typing, which includes an oligonucleotide

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RESULT 3
AAV16578/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alleles will be amplified and potentially detected by hybridisation with care probe. In the second stage, the group or basic type identified determines which set of allele specific primers will be used. The first of the two primers comprises an opt. labeled sequence common to each allele of the group identified in the first stage but different from other groups identified in stage one. The second primer may be a mixture of different labeled primers, complementary to two or more sequences within the group, or the amplification may be performed with only one second primer to detect the presence of a single group of alleles. In the third stage the specific allele is determined. This may be done by amplification or hybridisation using a radiolabelled probe. The method may be used for tissue matching, identifying disease susceptibility, etc. The method of the invention esp. distinguishes between DOB1*0304/DOB1*03032 and DOB1*0301/DOB1*0302.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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HLA-DR beta
HLA-DR beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           method comprises selectively amplifying the DNA of just one allele of the unknown pair and analysing the amplified DNA to determine which polymorphisms are present in that allele, and therefore assigning the unknown pair to the known type having that allele. The method comprise three test stages. The first stage is to establish the number of alleles present in each sample. Primers corresponding to fairly well conserved regions of a locus will increase the likelihood that unknown
                                                                                           Oligo:nucleotide probes and primers and particularly for tissue typing for bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV16578 standard; DNA; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                             Disclosure; Column 19; 20pp; English
                                                                                                                                           WPI; 1998-076408/07.
                                                                                                                                                                          Baxter-Lowe LA,
                                                                                                                                                                                                          (BLOO-)
                                                                                                                                                                                                                                         27-JUN-1990;
                                                                                                                                                                                                                                                                         08-APR-1993;
                                                                                                                                                                                                                                                                                                        30-DEC-1997.
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe G86 used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                major histocompatibility complex; HLA-DR; HLA-typing;
                                                                                                                                                                                                                                                                                                                                                                                                                                      consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; ilarity 100.0%; Conservative
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                                                                                                                                                                                                          CENT RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to identify HLA-DR sequences.
                                                                                                                                                                                                                                         90US-0544218
                                                                                                                                                                                                                                                                         93US-0057957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω
                                                                                                                                                                          Gorski JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; 7 C; 0 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                  us sequence; allelic polymorphism;
polymorphism; probe; bone marrow;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВP
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Pred. No. 1.9
D; Mismatches
                                                                                            methods
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                                                                                            s for HLA typing
transplants
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                                                                                                                                                                                                                                                                                                                                                                                                                    transplant;
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RESULT 4
AAF92638/c
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 Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probe which undergoes sequence-specific hybridisation with an HLA-DR beta consensus sequence at positions 61-64. The probe contains a labelling substance other than a nucleotide sequence, which facilitates detection of the probe. The HLA sequence of a subject is PCR amplified, and a probe that recognises an allelic polymorphism at a selected HLA locus is contacted with the amplified product. This first probe recognises a HLA-DR beta-allelic polymorphism. A second (different) probe is brought into contact with a second sample of the amplified DNA in a separate reaction, and hybridisation detected. The probes and primers are used for HLA typing, e.g. for tissue, especially bone
                                                                                       The present invention relates to human leukocyte antigen (HLA) typing. The method involves detecting polymorphic residues by sequence specific oligonucleotide probe hybridization (SSOPH) with labeled oligonucleotide probes.
                                                                                                                                                                                   Human leukocyte antigen typing by amplifying a sample followed by sequence specific oligonucleotide hybridization with labeled oligonucleotide probes that hybridize with a series of known control DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human;
SSOPH;
                                                                                                                                                                                                                                                                                                                            27-JUN-1990;
08-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLA-DR typing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF92638 standard; DNA; 12 BP
                                                                Sequence
                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                         Baxter-Lowe LA,
                                                                                                                                                                                                                                                                                                                                                                                                                     US6194147-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF92638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12 BP; 2 A; 0 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               marrow, transplants.
                                                                                                                                                                                 DNA sequences
                                                                                                                                                                                                                                                                                                  (BLOO-) BLOOD CENT RES FOUND
                                                                                                                                                                                                                                                                                                                                                                   30-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                             27-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 TCTCACCAACC
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                                                                                                                                                                                                                                                  2001-217923/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leukocyte antigen; HLA; typing; sequence specific probe;
                                                                12
                                                                BP;
                                                                                                                                                      Column 11-14; 16pp; English
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  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probe #18.
                                                                                                                                                                                                                                                                                                                           90US-0544218.
93US-0057957.
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                                                                                                                                                                                                                                                                         Gorski JA;
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            100.0%;
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                                                                                                                                                                                                                                                                                                    INC.
            Score 11; DB 22;
Pred. No. 1.9e+03
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Pred. No. 1.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 T; 0 other;
                                                               ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
 Mismatches
                                                               T; 0
                                                                other;
                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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                        Length 12;
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 Indels
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0;
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 Gaps
0;
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RESULT 6
AAQ26196/c
ID AAQ261!
XX
AC AAQ261!
XX

AAQ26196;

AAQ26196 standard; DNA;

16

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 Вþ
                      Qy
                                                                                                                 RESULT 5
AAQ26124/c
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                                                            Query Match
Best Local (
                                                  Matches
                                                                                                                                     The sequence is that of the hybridising region of tailed probe DRB15 for use in a method for determining HLA-DR beta sub-type in a nucleic acid sample. The method allows specific nucleic acid sequences of the second exon of HLA-DR beta genes to be amplified then probed for identification of polymorphic sequences. The amplified DNA is useful for typing homozgous or heterozygous samples from a variety of sources and for detecting allelic variants not distinguishable by serological methods. The typing system can be used in a reverse dot blot format which is simple and rapid to perform, produces detectable signals in minutes and can be utilised in tissue typing, determination of individual identity and isense susceptible individuals. Preliminary testing shows that the probe is more preferred than others. The probe is see also AAQ26092-Q26367.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Apple RJ,
Scharf SJ;
                                                                                                                                                                                                                                                                                                                                                          Method for determining HLA-DR beta sub-type in comprises amplification and hybridisation with primers, useful in tissue typing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9210589-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue typing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLA-DR beta sub-type tailed probe DRB15 hybridising region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ26124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ26124 standard; DNA; 16
                                                                                                                Sequence 16
                                                                                                                                                                                                                                                                                                                                 Example; Page 37;
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1992-234644/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HOFF ) HOFFMANN LA ROCHE & CO AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-DEC-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
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13
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                        1 tctcaccaacc 11
TCTCACCAACC
                                                             Similarity
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                                                                                                                B₽;
                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 identity determination; disease susceptible;
                                                                                                                2 A;
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                                                                                                                                                                                                                                                                                                                                  90pp; English.
                                                            100.0%;
                                                                                                                2 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bugawan
                                                                                                                8 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
                                                  0,
                                                             Score 11; DB 13;
Pred. No. 1.9e+03;
                                                                                                                4 T; 0 other;
                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Η,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>'1</u>
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                                                                          DB 13;
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                                                                                                                                                                                                                                                                                                                                                                      probes
                                                                                                                                                                                                                                                                                                                                                                                     DNA
                                                                        Length 16;
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                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                    sample
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                                                Gaps
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RESULT 7
ABL31303/c
ID ABL313
XX ABL313
AC ABL313
XX 21-MAR
XX 21-MAR
XX Human;
KW Immunc
XX Immunc
XX Humon §
KW Immunc
XX Homo §
XX PN WO2001
XX PO 06-DE(
XX
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                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 11
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              06-DEC-2001
                                                                                                                         Human HLA genotyping oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Method for determining HLA-DR beta sub-type in comprises amplification and hybridisation with primers, useful in tissue typing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apple :
Scharf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue typing; identity determination; disease susceptible; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HLA-DR beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-JAN-1993
                                      WO200192572-A1
                                                               Homo sapiens.
                                                                                     Human; human leukocyte antigen; immunogenetic; transplantation;
                                                                                                                                                     21-MAR-2002
                                                                                                                                                                             ABL31303;
                                                                                                                                                                                                   ABL31303 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example; Page 39; 90pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1992-234644/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-DEC-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                    See also AAQ26092-Q26367.
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                                                                                                                                                                                                                                                                TCTCACCAACC
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f SJ;
                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sub-type tailed
                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
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                                                                                                                                                                                                     DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΑB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROCHE & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                            100
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                                                                                                                                                                                                     ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probe DRB92 hybridising region
                                                                                                                                                                                                                                                                                                                            Score 11;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                          4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ą
                                                                                     HLA; genotype; p
genetic disease;
                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'TJ
                                                                                                                           SEQ ID NO 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Erlich
                                                                                                                                                                                                                                                                                                                          DB 13;
1.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HA,
                                                                                                                                                                                                                                                                                                                0;
                                                                                                  polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA sample probes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Griffith
                                                                                                                                                                                                                                                                                                                                      Length 16;
                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                               0;
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RESULT 8
AAQ26251/c
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       containing gene polymorphisms as alloantigens have been immobilised as primers for amplification of cleaved nucleic acids relating to gene polymorphisms. The method is useful for judging HLA genotypes of individuals by determining immunogenetic differences before transplanting between them, providing genetic information to decide compatibility of organ and tissue for transplantation e.g. of bone marrow, kidney, liver, pancreas, Langerhans islet in pancreas and cornea, susceptibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a typing kit for judging human leukocyte antigen (HLA) genotype of a sample by hybridising a substrate on which 10-24 base oligonucleotides (ABL30512-ABL31809) originating in the sequences of genes e.g. belonging to HLA class I antigens on human genome and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human leukocyte antigen (HLA) typir of individuals e.g. by determining transplanting between them -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
Method for determining HLA-DR beta sub-type in comprises amplification and hybridisation with
                                                       Apple RJ,
Scharf SJ;
                                                                                                                                                                                                                                                                       04-JAN-1993
                                                                                                                                                                                                                                                                                                                AAQ26251 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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                                  WPI; 1992-234644/28
                                                                                                              06-DEC-1990;
                                                                                                                                    06-DEC-1991;
                                                                                                                                                          25-JUN-1992
                                                                                                                                                                               WO9210589-A
                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                         Tissue typing;
                                                                                                                                                                                                                                               HLA-DR beta sub-type tailed
                                                                                                                                                                                                                                                                                           AAQ26251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inoko
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                                                                                        (HOFF ) HOFFMANN LA ROCHE & CO
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                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                  Begovich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP;
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genetic diseases
                                                                                                                                                                                                                         identity determination; disease susceptible; ss
                                                                                                             90US-0623098
                                                                                                                                    91WO-US09294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ν
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; 1 C;
                                                                                                                                                                                                                                                                                                                  DNA;
                                                                   AB,
                                                                                                                                                                                                                                                                    entry)
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                                                                  Bugawan T,
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                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                               probe DRB147 hybridising region
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       typing, useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and identifying individuals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 T;
                                                                                        ĀG
                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                         .
T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ng, useful for immunogenetic
                                                                                                                                                                                                                                                                                                                                                                                                                             No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0 other;
                                                                   Erlich HA,
                                                                                                                                                                                                                                                                                                                                                                                                                             DB 24;
1.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moriya
                                                                   Griffith RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           judging HLA
differences
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 16
                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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ices when
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DNA sample probes and

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RESULT ABL30817

ABL3081

ABL30817

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The invention relates to a typing kit for judging human leukocyte and (HLA) genotype of a sample by hybridising a substrate on which 10-24 oligonucleotides (ABL3012-ABL31809) originating in the sequences of genes e.g. belonging to HLA class I antigens on human genome and containing gene polymorphisms as alloantigens have been immobilised a primers for amplification of cleaved nucleic acids relating to gene polymorphisms. The method is useful for judging HLA genotypes of individuals by determining immunogenetic differences before transplan
                                                                                                                                                                                                                                       Claim 10; Page 151; 345pp;
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                                   The sequence represents a sequencing primer for DNA encoding the Fusari fungal enzyme, glucanase. Glucanase, endochitinase and exochitinase are polypeptides with cell-wall degrading activity, derived from Fusari fungal genes. The associated nucleic acids can be used to produce transgenic plants which are resistant to plant pathogens, particularly Fusarium species. They can also be used to isolate homologous genes fro fungi to obtain genes which protect host cells, including fungi, bacter and plants against related fungal pathogens. The polypeptides, especial chitinases and glucanases, are useful for degrading seafood waste, such as shells that contain chitin, or for chemical modification of chitin o
                                                                                                                                                                                                                                                                                                                                        (NOVO)
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 Sequence
                                                                                                                                                                                        Disclosure;
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                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                           Score 11; DB 24;
Pred. No. 1.9e+03;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pred. No. 1.9e+03;
mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                           4 T;
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                                                                                                                                                                                                                                                                                                                                                                                           0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               judging HLA
differences
                                                                                                                                                                                                                                                                                                         Length 18;
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                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               when
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                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                           0,
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ID XXX ACX
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AAQ06439/c
                                                                                                                                                                                                                                                                                                                                                                                        망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between them, providing genetic information to decide compatibility organ and tissue for transplantation e.g. of bone marrow, kidney, lipancreas, Langerhans islet in panoreas and cornea, susceptibility diagnosis of genetic diseases and identifying individuals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a typing kit for judging human leukocyte antigen (HLA) genotype of a sample by hybridising a substrate on which 10-24 base oligonucleotides (ABL30512-ABL31809) originating in the sequences of genes e.g. belonging to HLA class I antigens on human genome and containing gene polymorphisms as alloantigens have been immobilised as primers for amplification of cleaved nucleic acids relating to gene polymorphisms. The method is useful for judging HLA genotypes of individuals by determining immunogenetic differences before transplanting between them by determining immunogenetic differences before transplanting that the determining immunogenetic differences before transplanting the determining immunogenetic differences before transplanting that the determining immunogenetic differences before transplanting the determining immunogenetic differences before transplanting the determining immunogenetic differences before transplanting the determining the determining immunogenetic differences before transplanting the determining the
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                                                                                                                                               Oligonucleotide
                                                                                                                                                                                                                                                                             AAQ06439 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of individuals e.g. by dete
transplanting between them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human leukocyte antigen (HLA) Lyp...
                                                            Insulin-dependent diabetes; systemic Reiter's disease; ss.
                                                                                                                                                                                          04-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001; 2001WO-JP04662
                                                                                                                                                                                                                                      AAQ06439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-DEC-2001
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                                                                                                                             human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SYST-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunogenetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human;
                                                                                                                                                                                                                                                                                                                                                                                        14 TCTCACCAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            1 tctcaccaacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002-122074/16.
                                                                                                                      nucleotide probe
type I diabetes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human leukocyte antigen;
genetic; transplantation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYSTEM RES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kagiya T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 146; 345pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genotyping oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 2 A; 2 C; 9 G;
                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                         to a lamb
myelitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ichihara T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HLA) typing, useful
                                                                                                                                               lambda
                                                                                                                                                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 11; DB 24;
Pred. No. 1.9e+03;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLA; genotype; polymorphism;
genetic disease; ss.
                                                                                                                                               HLA-DR-5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matsumura Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ng, useful for immunogenetic
                                                                                lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID
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differences
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when
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RESULT 14
AAQ26219/c
ID AAQ26
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AC AAQ26:
DT 04-JA
XX Tiss
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Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe may be used in tests for proclivity towards autoimmune diseases such as insulin dependent diabetes, Reiter's disease Probes are highly specific, even able to differentiate between restriction fragments of identical size, and may also be used
                                      Method for determining HLA-DR beta sub-type in comprises amplification and hybridisation with primers, useful in tissue typing
                                                                                  WPI; 1992-234644/28.
                                                                                                      Apple RJ,
Scharf SJ;
                                                                                                                                                        06-DEC-1990;
                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                         Tissue typing; identity determination; disease susceptible; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Col 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DQ beta gene oligo:nucleotide(s) - for detection of proclivity in humans for development of type I diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1990-341710/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Owerbach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1986;
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                      Example; Page 40;
                                                                                                                                                                          06-DEC-1991;
                                                                                                                                                                                               25-JUN-1992.
                                                                                                                                                                                                                  W09210589-A
                                                                                                                                                                                                                                                                               HLA-DR beta
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                                                                                                                                                                                                                                                                                                                        AAQ26219;
                                                                                                                                                                                                                                                                                                                                           AAQ26219 standard;
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                                                                                                                                    (HOFF ) HOFFMANN LA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           typing.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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illarity 100.0
Conservative
                                                                                                                                                                                                                                                                              sub-type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 A;
  that of
                    90pp;
                                                                                                                                                                                                                                                                                                                                           DNA;
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                                                                                                                AΒ,
                                                                                                                                    ROCHE & CO
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С;
                                                                                                                                                                                                                                                                               tailed
 the hybridising region
                                                                                                                                                                                                                                                                                                                                           19
                      English.
                                                                                                               Bugawan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                               .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 G;
                                                                                                                                                                                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                             probe DRB115 hybridising region
                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 11; DE
Pred. No. 1.9
D; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 T;
                                                                                                                                    8
G
                                                                                                                                    H
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                                                                                                                Erlich
                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11;
1.9e+03;
                                                                                                               HA,
                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
  of tailed probe DRB115
                                                  DNA sample probes and
                                                                                                               Griffith RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     also be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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RESULT 15
AAX79408/c
ID AAX794
XX AAX794
XX AAX794
XX Tissue
KW Tissue
KW major
KW amplif
KW sequer
XX Synthe
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Best Local S
Matches 11
                             histocompatibility complex (MHC), esp. for typing donors for bone marrow transplants, involves determining if the donor tissue HLA-DR alleles are selected from the gp.: HLA-DRW5CC, DR13a,b, DR3a,n, DR5a-e, DRNewl, DR6a, DR8a-d, DRW55a-c, DR4a-f, DR7, DR9, DR2a-c B3, DR2a-d B1, DR10 and DR1a-c. The method uses PCR to amplify these regions followed by sequence-specific oligonucleotide probe hybridisation (SSOPH) using the probes AAX79365-X79429. SSOPH allows detection of polymorphisms that predict differences at a single amino acid level thus reducing errors and improving the chance of successfully matching tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for use in a method for determining HLA-DR beta sub-type in a nucleic acid sample. The method allows specific nucleic acid sequences of the second exon of HLA-DR beta genes to be amplified then probed for identification of polymorphic sequences. The amplified DNA is useful for typing homozgous or heterozygous samples from a variety of sources and for detecting allelic variants not distinguishable by serological methods. The typing system can be used in a reverse dot blot format which is simple and rapid to perform, produces detectable signals in minutes and can be utilised in tissue typing, determination of individual identity and identifying disease susceptible individuals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue typing; human leukocyte antigen; HLA; MHC; donor; allel major histocompatibility complex; bone marrow transplant; prim amplification; polymerase chain reaction; probe; polymorphism; sequence-specific oligonucleotide probe hybridisation; ss.
                                                                                                                                                                                                                                                                                A novel method of typing the human leukocyte antigen (HLA) of the major histocompatibility complex (MHC), esp. for typing donors for bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Improved method for HLA typing - by DNA amplification and sequence-specific oligo:nucleotide hybridisation, used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-JUN-1990;
08-APR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BLOO-) BLOOD CENT RES FOUND
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BI301500 UI-R-DLO-
BI552481 603256389
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ALIGNMENTS

ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS RESULT 1 AZ493433/c LOCUS DEFINITION FEATURES TITLE JOURNAL source Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 36)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts 84112 USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0328 row: A column: 12 Seq primer: CGTTGTAAAACGACGGCCAGT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah AZ493433 36 bp DN 1M0328A12F Mouse 10kb plasmid UUGC1M clone UUGC1M0328A12 F, DNA sequence. High quality sequence stop: Location/Qualifiers GSS. AZ493433 AZ493433.1 GI:10667114 Class: plasmid ends Mus musculus nouse mouse 308, Biomedical /organism="Mus musculus" /strain="C57BL/60" /db_xref="raxon:10090" /clone="UUGC1M0328A12" /clone_lib="Mouse 10kb plasmid UUGC1M library" Polymers Research Bldg., 36. NA linear GSS 05-OCT-2000 library Mus musculus genomic 20 S 2030 E., SLC, UŢ

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RESULT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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The first strand cDNA was primed with a biotinylated oligo-dT-NotI primer (5'-biotin-AACCCGGCTCGAGCGGCCGCTTTTTTTTTTTTTTTT-3').
                                                                             /tissue_type="pectoral muscle (after mastectomy)", /note="Vector: pcDNAII (Invitrogen); Site_1: BstXI; Site_2: Not1: The library was constructed by G. Lanfranchi. This library is not subtracted nor normalized.
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                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="s4000090D07"
/clone_lib="HM3"
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Seq primer: -40UP from Gibco
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              National Cancer Institute, Cancer Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ds cDNA was sonicated and size-selected in the range 350-550 bp. The 3' specific fragments were selected by streptavidin coated magnetic beads, ligated to non-palindromic BstXI adapters, NotI digested and directionally cloned into BstXI-NotI cut pcDNAII vector." a 11 c 21 g 24 t
                                                                                                                                                                                                                         /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated
                                                                                                                          constructed by Bento Soares and M. Fatima Bonaldo 27\ c 19\ g 24\ t
                                                                                                                                                                to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was
                                                                                                                                                                                                                                                                                                           /clone="IMAGE:1895656"
/clone_lib="NCI_CGAP_Lu5"
/tissue_type="carcinoid"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .100
                   100.0%;
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Pred. No.
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3E:1895656 3'
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63 TCTCACCAACC 73
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AA184061 108 bp mRNA linear EST 19 mo96f04.rl Stratagene mouse testis (#937308) Mus musculus clone IMAGE:567583 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: szhao@tigr.org

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC Library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Other_GSSs: RPCI-23-82M10.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Fraser, C.M.
Mouse BAC End Sequences from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 row: M column: 10
                                                                                                                                                                                                                                                                                                                                       /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH1DB electrocompetent cells (BRL Life Technologies). " a 18 c 17 g 30 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-82M10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RPCI-23"
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Tsegaye,G., Geer,K., Krol,M.,
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genomic clone
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                                               EST 15-FEB-1997
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Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                AA258662.1
EST.
                                                                                                                                                                                                 <code>zr61h08.r1</code> Soares_NhHMPu_S1 Homo sapiens cDNA clone 5', mRNA sequence. AA258662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FMAX: 314 400 2012
Email: mouseestévatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
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AA184061.1
                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                            Homo sapiens
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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1 (bases 1 to 108)
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/dev_stage="10-12 week old"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="Inbred CD-1"
/db_xref="taxon:10090"
/clone="IMAGE:567583"
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Homo.
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1 (bases 1 to 11)

Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Nagai,M.A., da Silva,W.A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOllveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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CM4-CT0639-220101-695-d02 CT0639 Homo sapiens
BG953134
                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WashU-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                          sequence tags
                                                                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed
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Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: -28ml3 rev2 ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1750 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
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+55-11-2704922
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                                                                                                                                       Natl. Acad. Sci. U.S.A.
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/db_xref="taxon:9606"
/clone="IMAGE:667935"
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/sscripts/gethtml2.pl?tl=CM4&t2=CM4-CT0639-
220101-695-d02&t3=2001-01-22&t4=1)
Seq_primer: puc 18 forward
                                                                                              This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&t2-MR2-HN0035-141200-015-e01&t3=2000-12-14&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deollyeira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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1 (bases 1 to 120)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
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BF828693
BF828693.1 GI:12173470
                                                                                                                                                                                                                         Tel: +55-11-2704922
Fax: +55-11-2707001
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                  primer: puc 18 forward
h quality sequence start: 10
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Location/Qualifiers
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/clone_lib="CT0639"
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                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.p1?t1-&t2-MR3-GN0029-110
900-004-f02_1&t3-2000-09-11&t4-1)
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1 (bases 1 to 122)

Dias Meto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
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MR3-GN0029-110900-004-f02_1 GN0029
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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             /note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A min1-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue mRNA and cDNA amplification were performed low stringency conditions."
31 c 38 g 22 t 1 others
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/dev_stage="Adult"
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/db_xref="taxon:9606"
                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                               /clone_lib="GN0029"
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SOURCE

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Matches

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RESULT 10
AA325418/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult (C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White (O., Sutton, G., Blake, J.A.), Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald (L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmarros, S.M., Merrick, J.M., Kelley, J.C., Liu, L.-I., Marmarros, S.M., Merrick, J.M., Shirley, R., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Bednarik, D.P., Cao, L., Cepeda, M.A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA325418
EST28422
AA325418
                                                                                                                                                                                                                                                                                                          Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         9712 Medical Center Drive, Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Institute for Genomic Research 9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA325418.1 GI:1977683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Initial assessment of human gene diversity and expression patterns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                  /note="Organ: brain; Vector: pBluescript SK-;
ECORI; Site_2: XhoI"
34 c 44 g 26 t 3 others
                                                                                         /tissue_type="cerebellum"
/dev_stage="adult"
                                                                                                                                         /db_xref="ATCC (inhost):125942"
/db_xref="taxon:9606"
/clone_lib="Cerebellum II"
                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                     M13 Reverse
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Pred. No.
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                                                                                                                                                                                                                                            TCTCACCAACC 52
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                                                                             HI040954 124 bp
CM3-NT0268-130201-748-d05_1 NT0268
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        BIO40954
BIO40954.1
                                                        sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trace considered overall poor quality 
Seq primer: -28ml3 rev1 ET from Amersham
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.
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/db_xref="taxon:966"
/clone="IMAGE:1183189"
/clone_lib="NCI_CGAP_Ew1"
/tissue_type="Ewing's sarcoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reference: Kri:
56:5380-5383."
a 18 c 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pAMP10; mRNA made from Ewing's sarcoma, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research
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1 (bases 1 to 124)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOllveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                   Mus musculus
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                          , DNA sequence. AZ753347
Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorg Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
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This sequence was derived from the FAPESP/LICR Human
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Fax: +55-11-2707001
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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130201-748-d05_1&t5=2001-02-13&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 119.
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/db_xref="taxon:9606"
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Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC
                                                                                  Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Researcl
9712 Medical Center Dr., Rockvilla
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                  Unpublished (1999)
Other_GSSs: RPCI-24-71F6.TJ
                                                                                                                                                                                                                                    Zhao,S., Nierman,W., Malek,J., Shatsman,S., Ak
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
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Other GSSs: RPCI-24-147P15.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
Department of Genomic Research
                                                                Email: szhao@tigr.org
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Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
plate: 147 row: P column: 15
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/clone_1b-"RPCI-24"
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/rectar de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
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Pred. No. 2.2e+04;
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Rockville,
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                                                                                                                        MD 20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
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    /lab_host="E.
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1 tctcaccaacc 11
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Plate: 71 row: F
Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                Other name: 02-KV2-3F4; date: 8/5/99; Submitted to the Database Expressed Sequence Tags (dbEST) on 08/25/99; More information is available at 'http://chrysie.tamu.edu/medicago'. Seq primer: SKmod (CTA gAA CTA gTg gAT CC).
                                                                                                                                                                                                                                                                                                                             College Station, TX 77843-3258, USA
Tel: 409 845 7707
Fax: 409 845 2891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolieae
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T113239e KV2 Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: VandenBosch | Department of Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 131)
VandenBosch, K., Hur
                                                                                                                                                                                                                                                                                                               Email: kate@mail.bio.tamu.edu
                                                                                                                                                                                                                                                                                                                                                                                                 Texas A&M University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Medicago truncatula
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enBosch,K., Hur,J., Moore,J., I
from Sinorhizobium-inoculated
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library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
/tissue_type="Seedling
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Pred. No. 2.2e+04;
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                  ling roots"
post-inoculation
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DNA clone
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e pKV2-1K8,
                       with
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coli strain SOLR"

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BASE COUNT
ORIGIN
Search completed: July 29, 2002, 23:22:49 Job time: 6825~{\rm sec}
                                                                                                                                                                                                                                                   Query Match 100.0%; Score 11; DB 9; Length 131; Best Local Similarity 100.0%; Pred. No. 2.2e+04; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                         1 teteaceaa¢c 11
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|112 TCTCACCAA¢C 102
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                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2: XhoI; CDNA was prepared from polyA+ enriched RNA. The CDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing CDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in SOLR cells." a X-3 g 53 t
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic search, using sw model
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length: 2000000000
            Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Issued_Patents_NA: *
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Gapop 10.0 , Gapext 1.0
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         US-08-025-038-16
US-08-050-073-17
US-08-050-073-191
US-08-050-073-23
US-08-050-073-191
US-09-441-346A-10
US-08-463-903-76
US-08-463-903-77
US-07-935-695-77
US-08-033-616-2
US-08-039-137-16
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US-08-050-073-15
US-08-050-073-15
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Sequence 16, Appl Sequence 17, Appl Sequence 1191, App Sequence 1191, App Sequence 1194, App Sequence 110, Appl Sequence 76, Appl Sequence 76, Appl Sequence 77, Appl Sequence 77, Appl Sequence 2, Appl Sequence 3, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 11, Appl Seq
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                                                                                                   Matches
                                                                                                                      Query Match
Best Local Similarity
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    1 tctcaccaacc 11
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2 TCTCACCAACC 12
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                                                                                                   Conservative
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Result No.

Score

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0 0 0 0 0 0 0 0 0 0 0 0 0 0

100.0%;

Score 11; DB 1; Pred. No. 2.7e+02;

Length 12; Indels

0,

Mismatches

0;

Gaps

0,

Database :

Minimum DB Maximum DB

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Scoring table: Sequence: Title: Perfect score:

Searched:

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US-08-050-073-69	US-08-050-073-53	US-08-050-073-52	US-08-050-073-48	US-08-050-073-46	US-08-050-073-45	US-08-050-073-43	US-08-050-073-39	US-08-050-073-38	US-08-050-073-36	US-08-050-073-34	US-08-050-073-33	US-08-050-073-29	US-08-050-073-25	US-08-050-073-24	US-08-050-073-23	US-08-050-073-21	US-08-050-073-20
Sequence 69, Appl	Sequence 53, Appl	`	`	`	Sequence 45, Appl	•	•	Sequence 38, Appl	Sequence 36, Appl	•	•	•	Sequence 25, Appl	Sequence 24, Appl	Sequence 23, Appl	•	Sequence 20, Appl

ALIGNMENTS

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: NUCLEIC ACID
STRANDEDNESS: single
; STOPOLOGY: linear
US-08-025-038-16
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                                                                                                                                                                            APPLICATION NUMBER: 07/544,218
FILING DATE: 27-UN-1990
ATTORNEY_AGENT INFORMATION:
NAME: Meyers, Philip G.
REGISTRATION NUMBER: 30,478
REFERENCE/DOCKET NUMBER: 204 854
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414)289-3761
                                                                                                                                      TELEFAX: (414)289-3791 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US
FILING DATE: 19930301
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 53202-5367
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BAXTER-LOWE, Lee-Ann
TITLE OF INVENTION: Method For HLA Typing
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 777 E. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wisconsin
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777 E. Wisconsin Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/025,038
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RESULT 2 US-08-050-073-77/c

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Petry Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 8769
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: NULLeic acid
STRANDEDNESS: Single
TOPOLOGY: linear
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                   Sequence 168, Application US/08050073 Patent No. 5567809
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Patent No. 5567809
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                  GENERAL INFORMATION:
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APPLICANT: LATER OF APPLICANT Griffith, Robert L.
APPLICANT: Scharf, Stephen J.
TITLE OF INVENTION: Methods and Reagents for HLA DRBeta DNA
TITLE OF INVENTION: Typing
TITLE OF SERUBNCES: 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,073
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Methods
TITLE OF INVENTION: Typing
NUMBER OF SEQUENCES: 315
CORRESPONDENCE ADDRESS:
                                                                                                                         APPLICANT: Apple, Raymond J.
APPLICANT: Begovich, Ann B.
APPLICANT: Bugawan, Teodorica L.
APPLICANT: Erlich, Henry A.
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APPLICANT: Erlich, He
APPLICANT: Griffith,
APPLICANT: Scharf, St
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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NTRY: U.S.A.
: 07110
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Bugawan, Teodorica L.
Frlich, Henry A.
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340 Kingsland Street
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Scharf, Stephen J.
VENTION: Methods and Reagents for HLA DRBeta DNA
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomic DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
2.7e+02;
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US-08-050-073-223/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 5567809
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 223, Application US/08050073 Patent No. 5567809
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LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 16
                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 87
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOR COMPATIBLE
COMPUTER: FOR COMPATIBLE
COMPUTER: FOR COMPATIBLE
COMPUTER: PACENTIA RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,
ATTORNEY/AGENT INFORMATION: NAME: Petry, Douglas A.
                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                        CITY: Nutley
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CITY: Nutley
                               CLASSIFICATION: 435
                                             FILING DATE:
                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                            STREET:
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                                                                                                                                                                                          New Jersey
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340 Kingsland Street
                                                                                                                                                                                                                                                          Griffith, Robert L.
Griffith, Stephen J.
Scharf, Stephen J.
WENTION: Methods and Reagents for HLA DRBeta DNA
NVENTION: Typing
SPOUENCES: 315
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Bugawan, Teodorica L.
Erlich, Henry A.
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                                                               US/08/050,073
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Pred. No. 2.7e+02;
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
US-08-050-073-223
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                                                                    us-08-050-073-191
                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 8769
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 191:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 191,
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Best Local
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Griffith, Robert L.
APPLICANT: Scharf, Stephen J.
TITLE OF INVENTION: Methods and Reagents for HLA DRBeta DNA
TITLE OF INVENTION: Typing
NUMBER OF SEQUENCES: 315
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Apple, Raymond J.
APPLICANT: Begovich, Ann B.
APPLICANT: Bugawan, Teodorica L.
APPLICANT: Erlich, Henry A.
APPLICANT: Griffith, Robert L.
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LENGTH: 17 base pairs
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                                                                                    MOLECULE TYPE:
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                                                                                                    STRANDEDNESS:
TOPOLOGY: 11
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nes 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U
ZIP: 07110
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                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
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5567809
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                                                                                                                                     nucleic acid
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                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                    genomic DNA
                                                                                                                  single
 100.0%;
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Pred. No. 2.7e+02;
 Score 11;
Pred. No.
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 DB 1; 1
2.7e+02;
                 Length 19;
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RESULT 7
US-08-758-306-1354/c
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; OTHER INFORMATION: Oligonucleotide ZC16,187
US-09-441-346a-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 580//...
Patent No. 580//...
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: MCSWiggen, James A.
AP
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LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
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PRIOR FILING DATE: 1999-11-16
PRIOR FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE:
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FILE REFERENCE: 98-34
CURRENT APPLICATION NUMBER: US/09/441,346A
CURRENT FILING DATE: 1999-11-16
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APPLICANT: Piddington, Christopher S
APPLICANT: Ellsworth, Jeff L.
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth
STREET: Suite 4700
                                                                                                                                          COMPUTER: IBM COMPONERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15
APPLICATION NUMBER: FILING DATE: Decemb CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
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                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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o. 5807743
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                                                                                                                        SYSTEM: IBM P.C. DO:
FastSeq Version 1.5
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                                                                                                                                                                                             IBM Compatible
                           December
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ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER: FILING DATE:

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RESULT 9
US-07-935-695-76/c
Sequence 76, Application US/07935695
; Patent No. 6329507
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                                                                                                                                                                                                                                     Query Match
Best Local Similarity
--+-hes 11; Conserve
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; NAME/KEY: 0101F primer
; LOCATION: 1..69
US-08-463-903-76
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/08/463,903
CURRENT FILING DATE: 1995-06-05
EARLIER APPLICATION NUMBER: US 07/935,695
EARLIER FILING DATE: 1992-08-21
NUMBER OF SEQ ID NOS: 102
SOFTWARE: MS-Word for Windows, Ver. 7.0
SEQ ID NO 76
LENGTH: 69
                                                                GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 76, Application US/08463903 Patent No. 6071515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Mezes) Peter S.
APPLICANT: Richard, Ruth A.
APPLICANT: Afforder, Joseph A.
APPLICANT: Kotité, Nicolas J.
APPLICANT: Kotité, Nicolas J.
TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
FILE REFERENCE: 40224A US
                                   APPLICANT:
                                                  APPLICANT:
 APPLICANT:
                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/132
TELECOMMUNICATION INFORMATION:
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LENGTH: 54 base pairs
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11 TCTCACCAACC 1
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TELEFAX: (213) 955-0440
TELEX: 67-3510
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                                                                                                                                                                                      TCTCACCAACC 31
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               Richard, Ruth A.
Affholter, Joseph A.
Kotite, Nicolas J.
                                                  Mezes, Peter S
                                                                                                                                                                                                                                                   100.0%; Score 11; DB 3; nilarity 100.0%; Pred. No. 2.9e+02; Conservative 0; Mismatches 0;
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nilarity 100.0%;
Conservative (
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Pred. No. 2.9e+02;
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APPLICANT:

Kotite, Nicolas

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RESULT 11
US-07-935-695-77
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; LOCATION: 1..74
US-08-463-903-77
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Best Local Similarity
Watches 11; Conserva
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                                                                  ; Sequence 77, Application US/07935695; Patent No. 6329507
GENERAL INFORMATION:
APPLICANT: Mezes, Petter S.
APPLICANT: Richard, Ruth A.
APPLICANT: Affholter, Joseph A.
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APPLICANT: Mezes, Peter S
APPLICANT: Richard, Ruth i
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Best Local Similarity
Matches 11; Conserv
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SEQ ID NO 76
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APPLICANT: Kotile, Nicolas J.
TITLE OF INVENTION: Dimer and Multimer Forms
FILE REFERENCE: 40224A US
CURRENT APPLICATION NUMBER: US/08/463,903
CURRENT FILING DATE: 1995-06-05
EARLIER APPLICATION NUMBER: US 07/935,695
EARLIER FILING DATE: 1992-08-21
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NAME/KEY: 0101F prime:
LOCATION: 1..69
COTHER INFORMATION: :
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CURRENT FILING DATE: 1992-08-21
PRIOR APPLICATION NUMBER: US 08/463,903
PRIOR FILING DATE: 1995-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 102
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SOFTWARE: MS-Word for Windows, Ver. 7.0
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                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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TYPE: DNA
ORGANISM: Artificial Sequence
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Conservative 0
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RESULT 12
US-08-933-616-2
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US-08-933-616-2
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Sequence 2, Application:
Parenal IMPORMATION:
Parenal IMPORMATION:
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SEQ ID NO 77
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Best Local :
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SOFTWARE: MS-Word for Windows, Ver. 7.0
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CURRENT FILING DATE: 1992-08-21
PRIOR APPLICATION NUMBER: US 08/463,903
PRIOR FILING DATE: 1995-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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                                                                                                                                        TELEFAX: (609) 466-2760 INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION: I
TITLE OF INVENTION: I
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                   REGISTRATION NUMBER: 32,538
REFERENCE/DOCKET NUMBER: UMD1-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 466-3407
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 04-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                    SEQUENCE CHARACTERISTICS:
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32 tctcaccaacc 42
                                                STRANDEDNESS:
TOPOLOGY: unl
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STATE: New Jersey
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nes 11; Conserv
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CLASSIFICATION:
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                                                                                                      LENGTH:
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                                                                nucleic acid
EDNESS: unknown
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                                                                                                  220 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Ralph C.
Cell-Type Specific Gene Transfer Using
Retroviral Vectors Containing Antibody-Envelope Fusion
Proteins and Wild-Type Envelope Fusion Proteins
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Pred. No.
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; LOCATION:
US-08-039-137-16
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Best Local S
Matches 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16,
                                                                      Query Match
Best Local
                                                         Matches
                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 14-APR-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: FAbian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE_POCKET NUMBER: 0550
TELECOMMUNICATION INFORMATION:
TELECHIONE: (415) 324-0860
TELECHIONE: (415) 324-0860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tilanus J.G., Marcel
TITLE OF INVENTION: Method of Determining a Genotype by
TITLE OF INVENTION: Comparing the Nucleotide Sequence of Members of a
:ent No. 5759771
                                                                                                                                                                                                 HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                           MOLECULE TYPE: cDNA to mRNA
 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patentl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                     INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                             TOPOLOGY:
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                           1 tctcaccaacc 11
                                                                                                                                                                                                                                                                                                    ENGTH:
TCTCACCAACC 237
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                                                                                                                                                                                                                                                                                                    268 base pairs
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N: 435
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Pred. No. 3.2e+02;
                                                                      Score 11;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                         Mismatches
                                                                   3.2e+02;
                                                                                     DB 1;
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                                                                                  Length 268;
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                                                         Indels
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RESULT 14 US-08-025-038-32/c ; Sequence 32, Application US/08025038

Patent No. 5545526
GENERAL INFORMATION:

APPLICANT: BAXTER-LOWE, Lee-Ann
TITLE OF INVENTION: Method For HLA Typing

46

CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear US-08-025-038-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                         Sequence 33, Application US/08025038
Patent No. 5545526
GENERAL INFORMATION:
APPLICANT: BAXTER-LOWE, Lee-Ann
TITLE OF INVENTION: Method For HLA Typing
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
COUNTRY: USA
ZIP: 53202-5367
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/025,038
FILING DATE: 19930301
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (414)289-3/91
INFORMATION FOR $EQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/025,038
FILING DATE: 19930301
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/544,218
FILING DATE: 27-JUN-1990
ATTORNEY/AGENT, INFORMATION:
NAME: Meyers, Philip G.
REGRENCELPOCKET NUMBER: 30,478
REFERENCELPOCKET NUMBER: 204 854
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 TCTCACCAACC 239
                                                                                                                                                                                                                              STATE: Wisconsin
                                                                                                                                                                                                                                               STREET: 777 E. v
CITY: Milwaukee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                            ADDRESSEE:
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777 E. Wisconsin Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 11; DB 1; 1
100.0%; Pred. No. 3.2e+02;
tive 0; Mismatches 0;
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                                                                                       Version #1.25
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Search completed: July 29, 2002, 23:56:14 Job time: 4755 sec
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                                                                                                                                          Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 11; Conservative 0
                                                                                                                                                                                                                                                                                                                        TELEFAX: (414)289-3791 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 269 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                    NAME: Meyers, Philip G.
REGISTRACE, NUMBER: 30,478
REFERENCE, DOCKET NUMBER: 200
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 27-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Philip G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                            1 tctcaccaacc 11
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249 TCTCACCAACC 239
                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                          (414)289-3761
                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07/544,218
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                                                                                                                                          Score 11; DB 1; L
Pred. No. 3.2e+02;
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                                                                                                                                                                         Length 269;
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Page 7

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                         /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT: *
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A. DAT: *
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B. DAT: *
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002. DAT: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

: 5	č	91000	אמינטון הפווקנוז טם	e119 c11		=======================================	
ဂ	1	6	100.0	10	16	AAQ99824	Loblolly pine fusi
ი	N	6	100.0	10	20	AAX59797	Primer OPC6 for fu
	ω	6	100.0	10	20	AAX23376	HLA-A, HLA-B, HLA-
	4	σ	100.0	10	21	AAC81828	Gerbera flavone sy
	σ	6	100.0	10	21	AAC81843	Gerbera flavone sy
	6	6	100.0	10	21	AAZ50866	Primer AP11 to ide
ი	7	6	100.0	10	21	AAZ77645	Human dendritic ce
	œ	6	100.0	10	21	AAZ77674	Human dendritic ce
ი	9	σ	100.0	10	21	AAZ78756	Human dendritic ce

4.5 4.5		c 42				c 38				c 34	33	c 32		30	29	c 28	27	26	c 25	24	c 23	22	21	20	c 19		17	c 16	15	14	c 13	12	_	c 10
6 100.0	100.	100.	100.	100.	100.	100		100	100	100	100	100	100	100	100	6 100.0						100	100	100	100	100	100	100		100	100	100.	100.	6 100.0
	12 13 AAQ24014	24	22	22 AAF4267	22		22	22	22	22 AAF4096	22	22	22	22	22 AAF3656	22 AAF3649	22	22	22	22	22	22	22	22	22	22	21	21	21	21	21 AAZ8281	21	21 AAZ7933	10 21 AAZ79193
Primer J Bam 12 us	Herpesvirus inhibi	Ωι	NORF gene	NORF gene	Yeast NORF gene SA	t NORF gene	t NORF		NORF gene	NORF gene	NORF gene		t NORF gene	NORF gene	NORF gene	t NORF gene	t NORF gene	NORF gene	NORF gene	NORF gene	NORF	Yeast NORF gene SA		C. cibarius SNGT2-	Human ubiquitously	Human ubiquitously	Metastatic breast	Metastatic breast	ic		tatic breas	tatic breas	dendritic	Human dendritic ce

ALIGNMENTS

RESULT 1 AAQ99824/c AAQ99824; AAQ99824 standard; cDNA; 10 BP

06-MAR-1996 (first entry)

Loblolly pine fusiform rust disease resistance marker OPC6 primer.

Lobbolly pine; Pinus taeda; fusiform rust disease; resistance marker; Cronartium quercum f.sp. fusiforme; Cqf; RAPD genetic marker; random amplified polymorphic DNA analysis; woody perennial plant; family selection; pedigree; mapping; primer; ss.

Synthetic.

W09519697-A1.

27-JUL-1995.

19-JAN-1995; 95WO-US00677

21-JAN-1994; 94US-0184567

Grattapaglia D, O'Malley DM, Sederoff RR;

(UYNC-) UNIV NORTH CAROLINA STATE.

WPI; 1995-269212/35.

Determn. of heritable oligogenic traits in woody plants by genomic

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RESULT
AAX59797,
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9797/c
AAX59797
                     The specification describes a method of identifying a genetic mark associated with a genetic locus conferring resistance to fusiform rust disease in a family of trees of the genus Pinus. The method comprises obtaining a sexually mature Pinus parent tree exhibiting
                                                                                                       genus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAPD analysis was used to study resistance to particular strains Cronartium quercuum f.sp. fusiforme (Cqf), the causative agent of fusiform rust disease, in loblolly pine (Pinus taeda). A putative heterozygous mother tree (clone 10-5) and two open pollinated daughters (half-sib clones 152-231 and 152-257) were crossed to a highly susceptible pollen parent. Progeny were challenged with inoculum from various aeciospore lines. It was found that the marker amplified by the 10-mer primer in AAQ99824 was predictive resistance to inoculation with single Aeciospore line 2-36 in
 resistance to fusiform rust trees of the parent by self
                                                                                Example
                                                                                                                                         WPI; 1999-347038/29
                                                                                                                                                              Amerson HV,
Sederoff RR,
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                                                                                                                                                                                                                                                                                                                            Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone 152-231 progeny. These and other results showed that resistance to fusiform rust disease in loblolly pine is under oligogenic control which can be mapped using genetic markers, using only a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mapping of multiple markers in a two generation plant family - to select plants with desired characteristics for breeding.
                                                                                                               Identifying
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                                                                                                                                                                                                                                  18-OCT-1995;
                                                                                                                                                                                                                                                         18-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                  tree family;
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94US-0184567.
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nus; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                   fusiform rust disease resistance marker.
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                                allele containing the target polymorphisms, (b) labelling the single-stranded nucleic acid molecules, immobilising oligonucleotide probes, each specific for a known polymorphism, on a support and (c) detecting fully complementary duplexes formed between the labelled single-stranded nucleic acid molecules and the immobilised probes. The method is used for determining differences and correspondences in polymorphisms between individuals, tissues or organs by comparing hybridisation patterns produced by the above method. The method uses probe arrays rather than requiring sequential hybridisation and removal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          progeny trees for a number of genetic markers, identifying genetic markers segregating in a Mendelian ratio and showing linkage with other genetic markers, measuring resistance to fusiform rust disease in multiple progeny trees and correlating the presence of resistance to fusiform rust disease with at least one marker identified in the previous step. The method is useful for determining the genetic basis previous step. The method is useful for determining the genetic basis
                                                                                                                                                    HLA-C allele by detecting polymorphisms using the primers AAX23371-X23380. The method involves (a) preparing single-strand nucleic acid molecules corresponding in sequence to the portion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     previous step. The method is useful for determining the genetic basis of resistance to fusiform rust disease and for producing trees of the Pinus genus that are resistant to the disease. The present primer was used in the method of the invention to identify and amplify resistance
                                                                                                                                                                                                                      Claim
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                                                                                                                                                                                           This invention
                                                                                                                                                                                                                                               polymorphism-specific
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                                                                                                                                     flavones that are useful as pharmaceuticals, e.g. in cancer treatment, as biologically active substances, e.g. to improve the immune defence system. Oligonucleotide fragments of (I) are used as probes and primers
                                                                                                                                                                     This invention describes a novel nucleic acid (I) that encodes flavone synthase II (FNSII) which has anticancer and immunomodulatory activity. FNSII catalyses conversion of naringenin to apigenin (I) is used to produce transgenic ornamental plants that have targeted alterations in flower color, also altered content/distribution of flavones in leaves, flowers and other tissues, e.g. increased resistance properties or symbbotic capacity. FNSII expressed by (I) is used in synthesis of
                                                                                                      Sequence
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                                                                                                                                                                                                                                                                 Example 4; Page 22; 40pp;
                                                                                                                                                                                                                                                                                                  New nucleic acid encoding flavone synthase II, useful e.g. for producing transgenic plants with altered flower color or flavone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
       Tobacco plant; salicylic acid inducible gene; sa-inducible gene; transgenic plant; pathogen
                                                                                                                                                                                                                                                                                                                          as biologically active substances, e.g. to improve the immune defence system. Oligonucleotide fragments of (I) are used as probes and primes or as antisense or ribozyme agents for regulating expression of (II).
                                                Primer AP11 to
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                                                                                                 AAZ50866;
                                                                                                                         AAZ50866 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding flavone synthase II, useful e.g. for producing transgenic plants with altered flower color or flavone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel nucleic acid (I) that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MART/) MARTENS (FORK/) FORKMANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-APR-1999;
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pharmaceutical; cancer; treatment; ss.
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3 ccgttc 8
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                                                                                                                                                                                                                                       Similarity 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transgenic plant; flavone synthase II; FNSII; anticancer;
                                                                                                                                                                                                                                                                                                     BP; 0 A; 4 C; 4 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fig 4B; 40pp; German
                                                                                                                                                                                                                                          Conservative
                                                                       (first
                                              identify tobacco salicylic acid inducible genes
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                                                                                                                           DNA;
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1.1e+05;
thes 0;
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fungal pathogen;
resistance; PCR

primer;

SS

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Best Local S
Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel salicylic acid inducible genes from tobacco plants, useful making transgenic plants with enhanced pathogenic resistance -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-AUG-1999;
                                                                                                                                                             SAGE tag; serial analysis of gene expression; antigen-presenting ce APC; monocyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL;
                                                                                                                                                                                                       Human dendritic cell SAGE tag,
                                                                                                                                                                                                                                                                                                                                                                                                                              SA-inducible
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                                                                                                                                                    T-lymphocyte;
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S-0089853.
S-0089878.
S-0089991.
3-0089992.
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Pred. No. 1.1
0; Mismatches
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1.1e+05;
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differentially expressed genes, or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell-rich sites, secretion of T cell growth factors and secretion of chemokines for
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19-JUN-1998;
19-JUN-1998;
                                                                                                                                                                                                     They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in an APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cell
                                                                                                                                                                                                                                                                                                                                                                              preferentially or differentially expressed in dendritic cells, while other transcripts correspond to novel genes. Antigen-presenting cell (APC)-associated costimulatory factors play an important role in the activation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone
                                                                                                                                                                                                                                                                                                                           insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory cofactors also being require for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated polynucleotides differentially expressed cells, useful in gene vaccines against cancer -
                                                                                                                                                                                                                                                                                                              sequences identified using the SAGE tags have several potential uses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESTs (expressed sequence tags) which were previously unknown to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             with monocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 65; 130pp; English.
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                                immune effector cells.
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antigen-presenting

gene

or

ng required Nucleic acid

Sequence 10 BP; A; 1 Ç 6 <u>ი</u> 0 U; 0 other;

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19-JUN-1998;
19-JUN-1998;
       Isolated polynucleotides differentially expressed in cells, useful in gene vaccines against cancer -
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                                                                                                                                                                                                                                                                                                                                                                                                          cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ77674 standard; DNA;
                               WPI; 2000-106077/09
                                                                                                                                                                                                                                                                                                                                           18-JUN-1999;
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8 CCGTTC 3
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) ROBERTS B L
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                                              Shankara
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Pred. No.
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      against
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAGE tag; serial analysis of gene expression; antigen presenting APC; monocyte-derived dendritic cell; differential gene expression immunostimulatory cofactor; costimulatory factor; CTL; cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer
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cc differentially expressed in monocyte-derived dendritic cells compared cc with monocytes, Some of the transcripts correspond to known genes or CC ESTs (expressed sequence tags) which were preferentially unknown to be preferentially or differentially expressed in dendritic cells, while CC (APC)-associated costimulatory factors play an important role in the cativation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone cells. Tumour activation of cytotoxic immune response that can cells is immune response that can cells sequences identified using the SAGE tags have several potential uses. CT They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen ce for agents that modulate expression of differentially expressed genes. Detection of these genes can be used in active inmunocyte lineage. Cells containing them are used in gene therapy. (or to stimulate cells containing them are used in gene therapy. (or co-administration of co-stimulatory signals, migration of chemokines for the presentation of co-stimulatory signals, migration of chemokines for the secretion of T cell growth factors and secretion of chemokines for the secretion of cell growth factors and secretion of chemokines for the secretion of cell growth factors and secretion of chemokines for the secretion of cell growth factors and secretion of chemokines for the secretion of cell growth factors and secretion of chemokines for the secretion of cell growth factors and secretion of chemokines for the secretion of cell growth factors and secretion of chemokines for the secretion of chemokines for the secretion of cell growth factors and secretion of chemokines for the secretion of chemokines for cells.
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   useful in gene vaccines against cancer -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         differentially expressed genes, or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell-rich sites, secretion of T cell growth factors and secretion of chemokines for
                                                                                                                                                                                          SAGE tag; serial analysis of gene expression; antigen-presenting ce APC; monocyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL;
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                                                                                                                                                                                                                                                                                                                                                                                                          AAZ79337 standard; DNA; 10 BP
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Claim 1; Page 115; 130pp; English.

vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell-rich sites, diagnosis, prognosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cell differentially expressed genes, or of their encoded proteins, can to identify cells as belonging to the monocyte lineage. Cells contained these genes can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and containing them. They may be used in vaccines to induce an immune response, particular against a tumour antigen; to modulate the genotype of an APC; to scree for agents that modulate expression of differentially expressed genes an APC; and as hybridisation probes/amplification primers for the insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acsequences identified using the SAGE tags have several potential uses. activation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone other transcripts correspond to novel genes. Antigen-presenting cell (APC)-associated costimulatory factors play an important role in the with monocytes. Some of the transcripts correspond to known genes or ESTs (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while Sequences AAZ77573-279709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared to abnormal particularly containing can be used to screen acid

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AAZ80767 to AAZ83941 represent tags corresponding to distinct
C transcripts that are preferentially transcribed in the metastatic breast
C tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the primary or non-metastatic
CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC cells). These transcripts can be used for diagnosis, prognosis,
CC monitoring and treatment of breast cancer, particularly where metastatic.
CD bignosis is by standard immunoassays or hybridisation/amplification
CC creactions. Compounds that modulate expression of the transcripts are
CC potentially useful for treatment of (metastatic) breast cancer, while
CC promoters from the transcripts are used to direct expression, in selected
CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC sequences), particularly an antigen-encoding sequence for use in gene or
CC cell-based vaccines. Polypeptides encoded by the transcripts are also
CC useful in vaccines; for diagnosing breast cancer and for raising
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prevention
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98US-0089997.
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1.1e+05;
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AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942 to AAZ86577 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense
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                                                                                                                                                                                  Claim 1;
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                                                                                                                                                                                                         Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer -
                                                                                                                                                                                                                                                                                    Roberts BL,
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        AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downzegulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequences), particularly an antigen-encoding sequence for use in cell-based vaccines. Polypeptides encoded by the transcripts are useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides therapeutic agents. Host cells that produce the polypeptides can to expand and isolate populations of educated, antigen-specific in effecter cells, e.g. cytotoxic T lymphocytes, and these used for
                                                                                                                                                  Isolated polynucleotides differentially and non-metastatic breast cancer cells, prevention and treatment of cancer -
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                                                                                                                                                                                                                                              SHANKARA S
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ROBERTS B L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
6; Conserv
                                                                                                                            Page 145; 219pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
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98US-0090040.
98US-0090041.
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hes 0;
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 of the
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RESULT 15
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19-JUN-1998;
19-JUN-1998;
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                                                                                                            and
                                                                                                                                          WPI;
                                                                                                                                                                                         (GENZ )
(ROBE/)
                                                                                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                                                                                                                                                  Human; metastatic breast tumour tissue; breast cancer; non-metastatic breast tumour tissue; gene therapy; antiantimetastatic; vaccine; diagnosis; ss.
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                                                                                                  prevention
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ROBERTS B
SHANKARA
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                                                                                                         polynucleotides differentially metastatic breast cancer cells,
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Pred. No.
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AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour

transcripts

be

used

Claim

1;

Page

150;

219pp;

English.

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Search completed: July 30, 2002, 00:01:19 Job time: 4930 sec
                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 6; DB 21; Length 10; Best Local Similarity 100.0%; Pred. No. 1.1e+05; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter cells; e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy.
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AZ653869 1M0527D14
AZ316663 1M0034G22
AZ436588 1M0224H20
AZ446206 1M0242106
AZ662500 1M0541G07
AZ789936 2M0038L17
AL467041 T. brucei
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AZ442576 1M0236K13
AZ621312 1M0454P19
AZ372925 1M0125D04
AZ819947 ZM0991E20
AL493847 T. brucei
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     T. brucei
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ORGANISM
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                               source
                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 682 Std Error: 0.00
Seg primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA911671 19 bp mRNA linear EST 10-
0149f08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1526823 3' similar to TR:018444 Q18444 COSMID C34D4.
Contains MSR1.b2 MSR1 repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 19)
                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                            /clone="IMAGE:1526823"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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TA119F03Q
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AZB09974 2M0074C18
AL451746 T. bruce1
AI748505 sb53h08 y
AZ780363 2M0017I11
AZB30168 2M0109E13
AL463256 T. bruce1
BG719541 602690991
BG719541 602699891
AI11841 uc14d10.r
AI174159 vz84e05.r
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AI17450 vz84e05.r

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AZ438586 1M0228E15
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RESULT 2
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1M0084L06F Mouse 10kb plasmid UUGCIM library
clone UUGC1M0084L06 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Roše, M., Roše, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0084 row: L column: 06
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse whole genome scaffolding with paired end reads from 10kb
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                         /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                   Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="uugC1M0084L06"
                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                  /sex="Male"
                                                                                                                                                                                                                                                                                                                                                   clone_lib="Mouse 10kb plasmid UUGC1M library"
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Pred. No.
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Err
Plate: 0078 row: M column: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Utah
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse whole genome scaffolding with paired end reads plasmid inserts % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
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AZ811866.1 GI:12980548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: CGTTGTAAAACGACGGCCAGT
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               (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel
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                                                                                                                                                                                             /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jack
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biomedical
electrophoresis.
                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="UUGC2M0078M08"
                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                          /sex="Male"
                                                                                                                                                                                                                                                                                                            /clone_lib="Mouse 10kb plasmid UUGC1M library"
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Std Error:
blumn: 08
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  Vector DNA
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6e+05;
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prepared
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from a derivative
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; Murinae; Mus
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0527 row: D column: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dunn, D., Aoyagi, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1M0527D14R Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC1M0527D14 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: CACACAGGAAACAGCTATGACC
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(bases 1 to 23)
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                                      (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                          /lab_host="E. Coli strain XL10-Gold, T1-resistant, /note="Vector: PMD42nv; Purified genomic DNA from musculus C57BL/6J (male) was obtained from the Jac Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biomedical Polymers Research Bldg.,
                        adaptored DNA was purified and size-selected
                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="C57BL/6J"
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/clone="UUGC1M0527D14"
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kb range using preparative agarose gel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0034 row: G column: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ316663 24 bp DNA linear GSS 29-SEP-200 1M0034G22R Mouse 10kb plasmid UUGCIM library Mus musculus genomic Clone UUGCIM0034G22 R, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
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University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biomedical Polymers Research Bldg.,
                                                                                                                                                                  Laboratory Mouse DNA Resource
                                                                                                                                                                                      /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0034G22"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                             /sex="Male"
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6.1e+05;
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University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0224 row: H column: 20
Seq primer: CGTTGTAAAACGACGGCCAGT
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Fax: 801 585 7177
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 with T4 DNA polymerase and T4 molymicleotide kinase. Adaptor oligonucleotides were molymicleotide kinase.
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                                                                                                                                                               /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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/clone="UUGC1M0224H20"
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/strain="C57BL/6J"
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B.
University of Utah
University of Utah
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4
                                                                                                         /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                        Laboratory Mouse DNA Resource
                                                                                                                                                                       /sex="Male"
                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="C57BL/6J"
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4
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                                                                                                                     /note="Vector: PWD42nv; Purified genomic DNA
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/strain="C57BL/6J"
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                                                                                                                                                                                             /sex="Male"
                                                                                                                                                                                                              /clone_lib="Mouse 10kb plasmid UUGC1M library"
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Pred. No.
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6.1e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ789936 24 bp DNA linear GSS 16-FEB-200 2M0038L17F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0038L17 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                  Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0038 row: L column: 17
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B. University of Utah University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ789936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biomedical Polymers Research Bldg.,
                                                                                              /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA
                                                                          Laboratory Mouse DNA Resource
                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="UUGC2M0038L17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                      /sex="Male"
                                                                                                                                             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                          /clone_lib="Mouse 10kb plasmid UUGC1M library"
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Pred. No.
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6.1e+05;
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nes 6; Conserv
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nhiesanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREUNA) (20Tat 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hi Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genomic survey sequence.
AL467041
AL467041.1 GI:11836396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 24)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                             Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
                                                                                                                                                                                                                                                                                                                                                           Email: nelsayed@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                       /organism="Trypanosoma k
/strain="TREU927"
/db_xref="taxon:5691"
/clone="143h10"
a 3 c 9 g 1
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a 10 c 5 g 5 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
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                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                CCGTTC
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AZ442576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trace considered overall poor quality Insert Length: 654 Std Error: 0.00 Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortlum/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)
Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 25)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Brn25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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M. Fatima

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Euteleostomi;

SOURCE ORGANISM

KEYWORDS VERSION

ACCESSION DEFINITION

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TITLE JOURNAL

BASE COUNT ORIGIN

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Insert Length: 10000 Std Error: (
Plate: 0236 row: K column: 13
Seq primer: CACACAGGAAACACCTATGACC
Class: plasmid ends
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Fax: 801 585 7177
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1 (bases 1 to 25)
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clone UUGC1M0236K13 R, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                 Conservative
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 Kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0236K13"
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/note="Yector: PWD42nv; Purified genomic DNA from M.
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erry
Plate: 0454 row: P column: 11
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University of Utah
Rm. 308, Biomedical
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Contact: Robert B.
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clone UUGC1M0454P19 F, DNA sequence.
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                                                                                          Conservative
                                                                                                                                                                                                                        was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pNAP42 (gil4732114 gblAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone="UUGC1M0454P19"
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/strain="C57BL/6J"
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nes 6; Conserv
16 CCGTTC 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
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Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ372925.1 GI:10486625
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                                                                                         Conservative
                                                                                                                                                                                                                (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pNASMIGHT (gil4732114)ghAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XI10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="UUGC1M0125D04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory Mouse DNA Resource
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100.0%; 5
tive 0;
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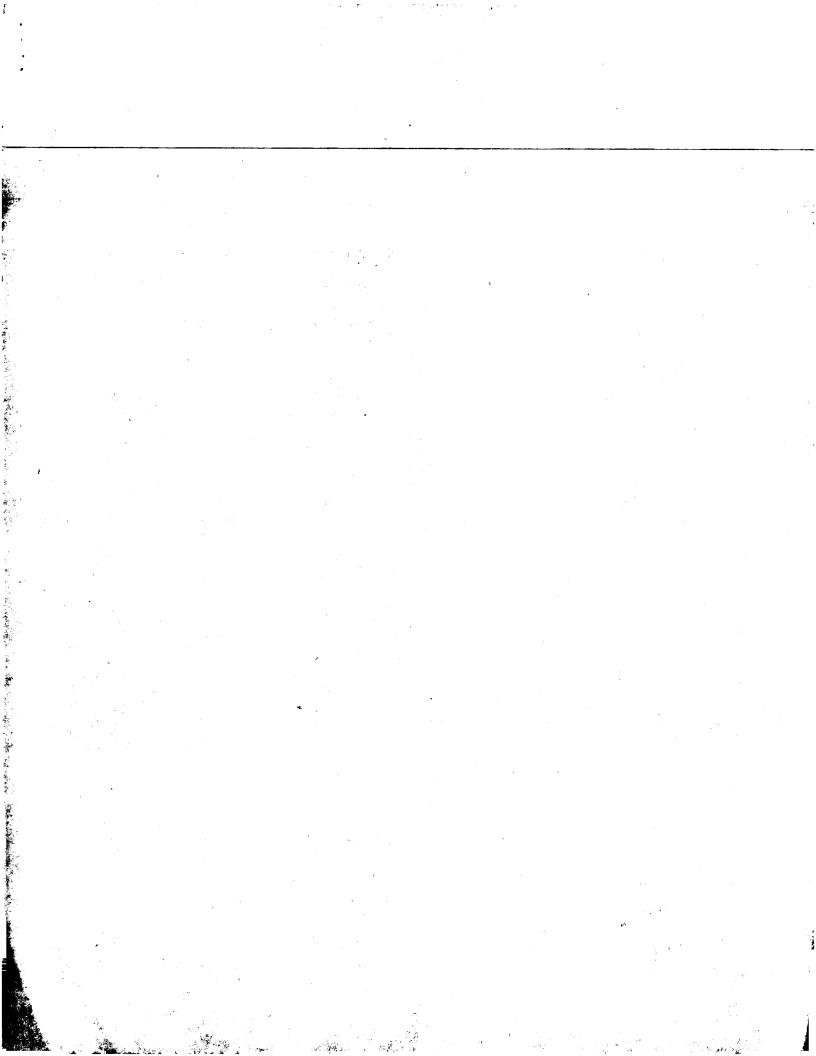
13 CCGTTC 1 ccgttc 6

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Contact: Robert B. We
University of Utah Ge
University of Utah
Rm. 308, Biomedical F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plate: 0091 row: E column: 20
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0091 row: E column: 20
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Fax: 801 585 7177
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  6;
                          Similarity
    Conservative
                                                                                                                                                                                                                                                                     /note="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynuclectide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114 jgb]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
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Post-processing: Minimum Match 0%
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US-07-879-470A-43	US-07-879-584A-43	US-07-879-647A-43	US-08-679-645-521	US-09-134-607A-3	US-09-118-317-14	US-08-942-673-14	US-08-696-834-15	US-08-513-841-14	5182195-49	PCT-US94-00265-14	US-09-054-832-26	US-09-078-954-17	US-08-486-403-6	US-08-464-514-6	US-09-402-764B-11	US-08-481-341-14	US-08-461-366A-4
Sequence 43, Appl	Sequence 43, Appl	Sequence 43, Appl	Sequence 521, App	Sequence 3, Appli	Sequence 14, Appl	Sequence 14, Appl		Sequence 14, Appl	Patent No. 5182195	Sequence 14, Appl	Sequence 26, Appl	Sequence 17, Appl	Sequence 6, Appli	Sequence 6, Appli	`	14	Sequence 4, Appli

ALIGNMENTS

; LENGTH: 9 base pairs ; TYPE: nucleic acid ; STRANDEDNESS: both ; TOPOLOGY: both ; MOLECULE TYPE: DNA US-08-642-045B-2 US-08-642-045B-2/c ATTORNEY/AGENT INFORMATION: NAME: DeLuca, Mark REGISTRATION NUMBER: 33,229 REFERENCE/DOCKET NUMBER: APOL TELECOMMUNICATION INFORMATION: TELEPHONE: 215-568-3100 TELEPAX: 215-568-3439 INFORMATION FOR SEQ ID NO: 2: Patent No. 5851804 GENERAL INFORMATION: Sequence 2, Application US/08642045B Patent No. 5851804 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: WINDOWS SOFTWARE: WORDPEFECT 6.0/6.1 APPLICANT: Snyder, Linda A. APPLICANT: Satishchaodran, C. TITLE OF INVENTION: CHIMERIC KANAMYCIN RESISTANCE GENE NUMBER OF SEQUENCES: 25 CORRESPONDENCE ADDRESS: ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5851804ris STREET: One Liberty Place, 46th floor CURRENT APPLICATION DATA: SEQUENCE CHARACTERISTICS: STREET: One Liberty F CITY: Philadelphia STATE: Pennsylvania COUNTRY: USA ZIP: 19103 APPLICATION NUMBER: FILING DATE: 06-MAN CLASSIFICATION: 51 06-MAY-1996 US/08/642,045B APOL-0262

Query Match Best Local Similarity

100.0%;

Score 6; Pred. No.

DB 2; L 2.5e+07;

Length 9;

Matches

Conservative

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Gaps

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US-08-852-268-4/c
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                                                                                                                                                                                 Sequence 8, Application US/08545253A Patent No. 5908978
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                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                              GENERAL INFORMATION:
APPLICANT: O'Malley, David M.
APPLICANT: Sederoff, Ronald R
APPLICANT: Grattapaglia, Dari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Pachuk
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: CHAIN REACTION CLONING NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOORDOO'S
STREET
                              APPLICANT: E. GEORGE KUhlman
TITLE OF INVENTION: METHODS FOR WITHIN FAMILY
TITLE OF INVENTION: SELECTION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: DeLuda, Mark
REGISTATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: APR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215,568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 06-MAY-1996
CLASSIFICATION: 435
             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
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                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: WINDOWS
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                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                  8 CCGTTC 3
                                                                                                                                                                                                                                                                                                             1 ccgttc 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 base pairs
                                                                                                            Sederoff, Ronald R. Grattapaglia, Dario
                                                                              Henry V. Amerson
Phillip Wilcox
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WOODY PERENNIALS USING GENETIC MARKERS 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US 08/642,045
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Query Match
Best Local Similarity
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US-08-719-337-8/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: cDNA US-08-545-253A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/08719337 Patent No. 6054634
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: O'Mailey, David M. APPLICANT: Sederroff, Ronald R. APPLICANT: Grattapaglia, Dario TITLE OF INVENTION: METHODS FO TITLE OF INVENTION: MOODY PERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFOMMUNICATION INFORMATION:
TELEPHONE: (919) 881-3140
TELEFAX: (919) 881-3175
                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 50
                                CLASSIFICATION: 047 PRIOR APPLICATION DATA:
                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
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                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Post Office Drawer 340
CITY: Charlotte
STATE: No. 5908978th Carolina
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CITY: Charlotte
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CLASSIFICATION:
APPLICATION NUMBER: 08/1 FILING DATE: 21-JAN-1994
                                                                    APPLICATION NUMBER: FILING DATE: 25-SE
                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                        28234
                                                                                                                                                                                                                                                       No. 6054634th Carolina
                                                                                                                                                                                                                                                                                                                                                         Grattapaglia, Dario
NVENTION: METHODS FOR WITHIN FAMILY SELECTION IN
NVENTION: WOODY PERENNIALS USING GENETIC MARKERS
                                                                                                                                                                                                                                                                                             Post Office Drawer 34009
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                                                                      25-SEP-1996
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                                                                                         US/08/719,337
                 08/184,567
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RESULT 6
US-07-974-447-10
                                                                                                                                                                                          TOPOLOGY: US-08-878-835A-7
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Best Local Similarity 100.0%;
Matches 6; Conservative 0
                                                                                                                    Matches
                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PO 0605
FILING DATE: 21 June 1996
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (919) 881-317
TELEX: 575102
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible w/ Pentium Processor OPERATING SYSTEM: Microsoft Windows 95 SOFTWARE: Microsoft Word 97 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 10
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: William Mitchell Molyneux
                                                                                                                                                                                                                    TYPE: Nucleic Acid
STRANDEDNESS: Doub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: The STATE: Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/878,835A FILING DATE: June 19, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 50:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Sibley, Kenneth D. REGISTRATION NUMBER: 31,
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                                                                                   1 ccgttc 6
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The Baker Building - Sixth Floor 1940 East 6th Street
                                                                                                                  Conservative
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                                                                                                                                                                                                        Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                          3.5 inch, 1.44 MByte storage
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Pred. No.
                                                                                                                                Score 6;
Pred. No.
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RESULT 7
US-08-149-199-10
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Best Local Similarity
"-* hes 6; Conserva"
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; MOLECULE TYPE:
US-07-974-447-10
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                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08149199 Patent No. 5501964
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                                                                                                                                                                                                                                  Patent No. 3042.

GENERAL INFORMATION:

APPLICANT: Wigler, Michael H

APPLICANT: Lisitsyn, Nikolai

APPLICANT: Lisitsyn, Nikolai

APPLICANT: Lisitsyn, Nikolai

AREPRESENTATIONAL APPROACH TO GENOMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 781-1
TELEFAX: (415) 398-324
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PCDOS/MSDOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROwland, Bertram I
REGISTRATION UNMBER: 20,015
REFERENCE/DOCKET NUMBER: A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

EDDIN TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: A REPRESENTATIONAL APPROACH TO GENOMIC TITLE OF INVENTION: ANALYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wigler, Michael H
APPLICANT: Lisitsyn, Nikolai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                      COUNTRY: USA
ZIP: 941114187
                                                                                                                                     CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/07/974,447 FILING DATE: 12-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                            STREET:
                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                            ### 4 Embarcadero Center,
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                                                                                                                                                                              TEST, ALBRITTON & HERBERT
er, Suite 3400
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CURRENT APPLICÁTION DATA:
APPLICATION NUMBER: US/08/149
FILING DATE: 9-No. 5501964-93
CLASSIFICATIÓN: 435

US/08/149,199

ATTORNEY/AGENT INFORMATION:

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RESULT 8

US-08-411-727-5/c

; Sequence 5, Application US/08411727

; Patent No. 5705161

; Patent No. 5705161 5683703
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
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APPLICANT: VAN DER

APPLICANT: POOLMAN

APPLICANT: HOOGERH
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Matches 6; Conserv
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                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: NL 9201716
FILING DATE: 02 OCT-1992
PRIOR APPLICATION NUMBER: WO PCT/NL93/00163
APPLICATION NUMBER: WO PCT/NL93/00163
FILING DATE: 30-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A57438/BIR CSHL002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 7811989
TELEFAX: (415) 3983249
TELEFAX: (415) 3983249
                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IPM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 1: MOLECULE TYPE:
REFERENCE/DOCKET NUMBER: BO TELECOMMUNICATION INFORMATION: TELEPHONE: 703-521-2297 TELEPHONE: 703-685-0573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: IMMUNOGENIC MENINGOCOCCAL LPS AND OTHER TITLE OF INVENTION: MEMBRANE VESICLES AND VACCINE THEREFROM
                                                                           NAME: PATCH Andrew J. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/411,727 FILING DATE: 01-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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Y: U.S.A.
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POOLMAN, Jan Theunis
HOOGERHOUT, Peter
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ilarity 100.0%;
Conservative (
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Pred. No. 1.6
0; Mismatches
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1.6e+04;

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; TOPOLOGY: li
; MOLECULE TYPE:
US-08-411-727-5
                                                                  ; TOPOLOGY: 1; MOLECULE TYPE: US-08-411-727-6
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Patent No. 5705161
Patent No. 5705161 5683703
GENERAL INFORMATION:
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Query Match
Best Local Similarity
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Matches 6; Conserv
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                                                                                                                                                                                     TELEX: 248425 EMBON INFORMATION FOR SEQ ID NO:
                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: NL 9201716
FILING DATE: 02-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/NL93/00163
FILING DATE: 30-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: VAN DER LEY, Peter Andre
APPLICANT: POOLMAN, Jan Theunis
APPLICANT: HOOGERHOUT, Peter
TITLE OF INVENTION: IMMUNGENIC MENINGOCOCCAL LPS AND OTHER
TITLE OF INVENTION: MEMBRANE VESICLES AND VACCINE THEREFROM
                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-521-2297
TELEFAX: 703-685-0573
                                                                                                                                                                                                                                                                                                                      FILING DATE: 30-JUL-1993 ATTORNEY/AGENT INFORMATION:
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COUNTRY:
                                                                                                                                                                                                                                                                    NAME: PATCH, Andrew J. REGISTRATION NUMBER: 329
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/411,727 FILING DATE: 01-MAY-1995
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                  nucleic acid
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Y: U.S.A.
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                                                                                  DNA (genomic)
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 Score 6;
Pred. No.
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Pred. No.
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                 DB 1;
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US-08-858-767-8
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
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                                                                                                     Sequence 8, Application US/08858767 Patent No. 5837468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 5837468
                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                       Query Match
Best Local S
                                                                    GENERAL INFORMATION: APPLICANT: WANG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,767
FILING DATE: 19-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite
APPLICANT: DUVICK, Jonathan P. APPLICANT: BRIGGS, Steven P. TITLE OF INVENTION: PCR-BASED TITLE OF INVENTION: METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 33229/325/PIHI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/481,687 FILING DATE: 07-JUN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DUVICK, Jonathan P.
APPLICANT: BRIGGS, Steven P.
TITLE OF INVENTION: PCR-BASED (
TITLE OF INVENTION: METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nuclei
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: BENT, Stephen A REGISTRATION NUMBER: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX:
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                                                                                                                                                                                                        CCGTTC 9
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nilarity 100.0%;
Conservative 0
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                                                                    WANG, Xun
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                                                                                                                                                                                                                                                                                                                                                                           linear
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                 PCR-BASED CDNA SUBTRACTIVE CLONING
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hes 0;
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Matches
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INFORMATION FOR SEQ ID NO:
                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 33:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                               TITLE OF INVENTION: PC.
TITLE OF INVENTION: ME
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                     APPLICANT: DUVICK, Jonathan P. APPLICANT: BRIGGS, Steven P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                      APPLICANT: WANG, Xun
                                                                                                                                                                                   STREET: 3000 K S CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 100.0%; Score 6; DB Local Similarity 100.0%; Pred. No. 1.1 tes 6; Conservative 0; Mismatches
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                                                                                                                                                                    COUNTRY:
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 CLASSIFICATION: 435
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3000 K Street, N.W., Suite 500
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SYSTEM: PC-DOS/MS-DOS
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19-MAY-1997
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                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNUMBER: US/08/858,767
FILING DATE: 19-MAY-1997
APPLICATION NUMBER: US 08/481,687
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
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INFORMATION FOR SEQ ID NO:
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REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3322
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
               INFORMATION FOR SEQ ID NO:
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                                                                              REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 33
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 SEQUENCE
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APPLICANT: DÜVICK, Jonathan P.
APPLICANT: BRIGGS, Steven P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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CITY: Washington
STATE: D.C.
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nes 6; Conserv
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TYPE: nucleic acid
STRANDEDNESS: single
                                  TELEX:
                                              TELEFAX:
                                                                 TELEPHONE:
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                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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20007-5109
CHARACTERISTICS:
                                904136
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                                                : (202)672-5300
(202)672-5399
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100.0%; F
tive 0;
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Pred. No.
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APPLICANT: Widler, Michael
APPLICANT: Lisitsyn, Nikolai
TITLE OF INVENTION: A REPRESENTATIONAL APPROACH TO DNA ANALYSIS
FILE REFERENCE: CSHL.002.04US
CURRENT APPLICATION NUMBER: US/09/261,079
CURRENT FILING DATE: 1999-03-02
EARLIER APPLICATION NUMBER: 08/478,242
EARLIER FILING DATE: 1995-06-07
EARLIER FILING DATE: 1995-11-12
VERNITER FILING DATE: 1992-11-12
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VEY. 2.0
SOFTWARE: PATENTIN VEY. 2.0
LENGTH: 12
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Best Local Similarity
Whethes 6; Conserva
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; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: OLIGONUCLEOTIDE
US-09-115-061-10
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; STRANDEDNESS: sing;
TOPOLOGY: linear
US-08-863-028-8
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US-09-261-079-10
                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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SEQ ID NO 10
LENGTH: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: 08/149,199
EARLIER FILING DATE: 1993-11-09
EARLIER APPLICATION NUMBER: 07/974,447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wigler, Michael APPLICANT: Lisitsyn, Nikolai TITLE OF INVENTION: A REPRESENTATIONAL APPROACH TO DNA ANALYSIS FILE REFERENCE: CSHL.002.03US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
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TYPE: n
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 6;
Pred. No.
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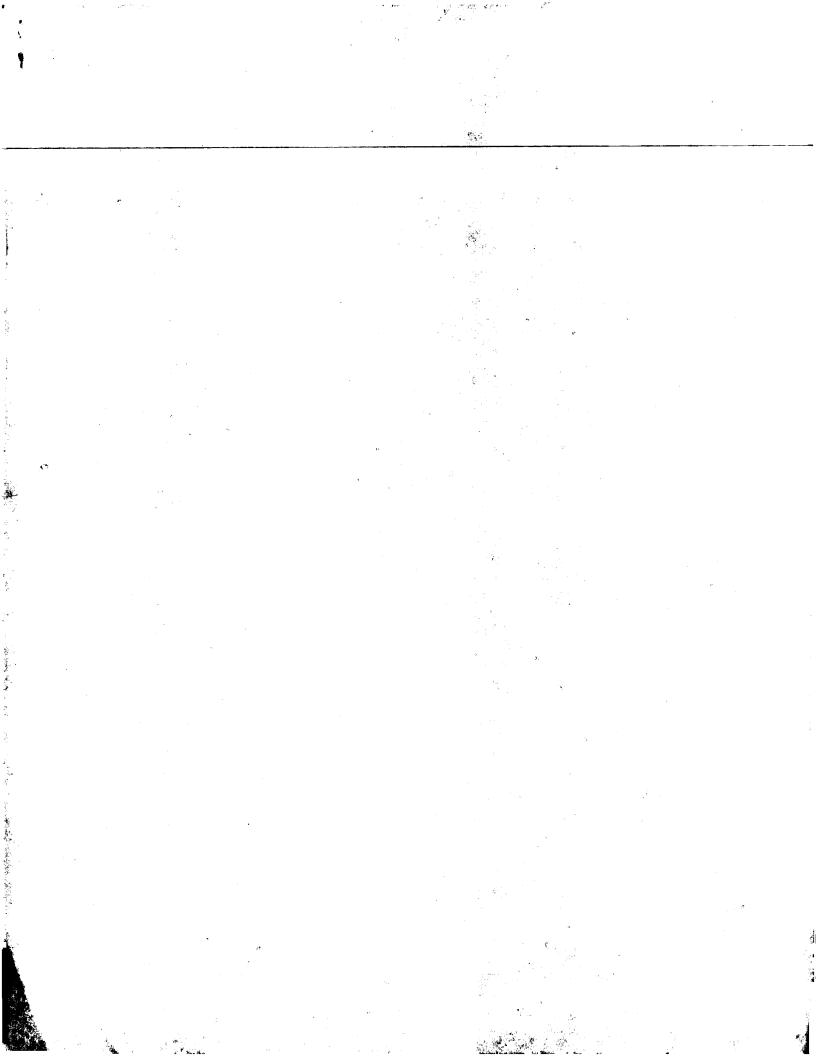
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: TYPE: DNA
: ORGANISM: Attificial Sequence
: DNAMES: DNAMISM: Attificial Sequence:
: OTHER INCOMPATION: OLGONOCLEOTIDE

US-09-261-079-10

Query Matches 6; Conservative 0; Fred: No. 1.6s+04;
MATCHES 6; CONSERVATIVE 0; Mismatches 0; Indels 0; Gaps 0;
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Search completed: July 29, 2002, 23:56:14

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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A01751 DNA fragmen
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A89485 Sequence 11
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RESULT 1
AR070974/c
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                          1 (bases 1 to 10)
Amerson,H.V., Wilcox,P., Sederoff,R.R., Ku O'Malley,D.M. and Grattapaglia,D.
Methods for within family selection of diperennials using genetic markers
perennials using genetic markers
patent: US 5908978-A 8 01-JUN-1999;
Location/Qualifiers
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AR070974
AR070974.1 GI:7221862
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 10)
Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
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Martens,S. and Forkmann,G.
Genetic sequence which codes for the
use of the same
Patent: WO 0065073-A 11 02-NOV-2000;
Martens, Stefan (DE) ; Forkmann, Ger
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Sequence 11 from Patent WO0065073
AX043779
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Patent: WO 0138577-A 320 31-MAY-2001;
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AX152684
A38146 12 bp
Sequence 2 from Patent WO9408021.
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Location/Qualifiers
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Patent: WO 0138577-A 599 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                            Wang, X., Duvick, J.P. and Briggs, S.P. PCR-based CDNA substractive cloning Patent: US 5837468-A 6 17-NOV-1998; Location/Qualifiers
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AR055101
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Van,D.L., Poolman,J.T. and Hoogerhout,P.
IMMUNOGENIC MENINGOCOCCAL LPS AND OUTER MEMBRANE VESICLES
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Sequence 8 i
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                                               Wang,X., Duvick,J.P. and Briggs,S.P. PCR-based cDNA subtractive cloning material US 5853991-A 8 29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                   Wang,X., Duvick,J.P. and Briggs,S.P.
PCR-based cDNA subtractive cloning method
Patent: US 5853991-A 6 29-DEC-1998;
Location/Qualifiers
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Sequence 6 from patent
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Wang, X., Duvick, J.P. and Briggs, S.P.
PCR-based cDNA substractive cloning
Patent: US 5837468 A 8 17-NOV-1998;
Location/Qualifiers
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Patent: US 6159713-A 10 12-DEC-2000;
Cocation/Qualifiers
1. .12
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Wigler, M. and Lisitsyn, N.
                                                                                                                                         genomic sequences
Patent: US 5436142-A 10 25-JUL-1995;
Location/Qualifiers
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Wigler, M. and Lisitsyn, N.
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Holesek, J.J. and Mamone, A.J.
Method and reagent for inhibiting viral replication
L patent: JP 200342285-A 95 12-DEC-2000;
RIBOZYME PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2000342285-A/95
PD 12-DEC-2000
PF 01-MAY-2000 JP 2000132616
PR 11-MAY-1992 US 07/882689,14-MAY-1992 US 07/882712
14-MAY-1992 US 07/88282713,14-MAY-1992 US 07/88282
14-MAY-1992 US 07/882831,14-MAY-1992 US 07/88282
14-MAY-1992 US 07/882886,14-MAY-1992 US 07/88282
14-MAY-1992 US 07/882889,14-MAY-1992 US 07/88282
14-MAY-1992 US 07/88289,14-MAY-1992 US 07/88282
14-MAY-1992 US 07/88289,14-MAY-1992 US 07/88281
14-MAY-1992 US 07/88289,14-MAY-1992 US 07/884931
14-MAY-1992 US 07/883849,14-MAY-1992 US 07/88433
14-MAY-1992 US 07/884427,14-MAY-1992 US 07/88433
14-MAY-1992 US 07/884427,14-MAY-1992 US 07/88433
14-MAY-1992 US 07/884436,14-MAY-1992 US 07/884433
14-MAY-1992 US 07/98332,07-DEC-1992 US 07/987133
07-DEC-1992 US 07/98332,07-DEC-1992 US 07/987133
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JP 2000342285-A/95.
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Patent: US 5501964-A 10 26-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    artificial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 14)
                                                                                                                          JAMES J HOLESEK, ANTHONY J MAMONE C12N15/09, C12N5/10, C12N7/00, C12N9/22//(C12N5/10, C12R1:91),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                            Key
                                                                                      C12N5/00, (C12N5/00, C12R1:91)
                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
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10 from patent US 5501964.
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1. .12
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3 c 3 g
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17882713,14-MAY-1992 US
177882713,14-MAY-1992 US
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177882713,14-MAY-1992 US
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177884436,14-MAY-1992 US
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177884436,14-MAY-1992 US
17798338,26-AUG-1992 US
1779337130,07-DEC-1992 US
177987130,07-DEC-1992 US
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                                          Location/Qualifiers
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Pred. No. 1.6
0; Mismatches
/organism='Artificial Sequence'
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J. 1.6e+06;
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07/882714 PR
07/882824 PR
07/882886 PR
07/882921 PR
07/882823 PR
07/884073 PR
07/884431 PR
07/884431 PR
07/884431 PR
07/884431 PR
07/884359 PR
07/987133 PI
07/987133 PI
UGEN, PI DENNIS G
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BASE COUNT
ORIGIN
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BD001364
LOCUS
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AUTHORS
                                                                                                                                                                          FEATURES
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 6; Conservative 0; Mismatches 0;
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                                                                                                                                     source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Draper K.G., Dadyktz,L.W., Macswigen,J.A., Maysejak,D.G.,
Holesek,J.J. and Mamone,A.J.
Method and resegent for inhibiting viral replication
Patent: JP 2000342286-A 95 12-DEC-2000;
RIBOZYME PHARMACEGUTICALS INC
OS Artificial Sequence
PN JP 2000342286-A/95
PE 01-MAY-2000 JP 2000132651
PF 01-MAY-1992 US 07/882713,14-MAY-1992 US 07/882714 PR
11-MAY-1992 US 07/88273,14-MAY-1992 US 07/88274 PR
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14-MAY-1992 US 07/882889,14-MAY-1992 US 07/88283 PR
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14-MAY-1992 US 07/884462,14-MAY-1992 US 07/88433 PR
14-MAY-1992 US 07/884425,14-MAY-1992 US 07/88431 PR
14-MAY-1992 US 07/884436,14-MAY-1992 US 07/88431 PR
14-MAY-1992 US 07/98323,07-DEC-1992 US 07/987133 PI
15-OCT-1992 US 07/987130,07-DEC-1992 US 07/987133 PI
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CC
FH Key
FT Source
                                                                                                                                                                                                                                                                                                                                                                                                          MAYSEJAK,
PI JAME
PC C12N
PC A61K
PC A61K
PC A61K
PC A61P
PC A61P
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1 (bases 1 to 14)
                                                                                                                                                                                                                                                                                                                                                                  A61P31/14,A61P31/16,A61P31/18,A61P31/22,A61P35/02,C1201/68, PC (C12N15/09,C12R1:93),C12N15/00,C12N5/00,A61K37/48,(C12N15/00, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                JAMES J HOLESEK, ANTHONY J MAMONE
C12N15/09,C12N5/10,C12N7/00//A61K38/43,A61K39/125,A61K39/13,
A61K39/135,
A61K39/145,A61K39/21,A61K39/23,A61K39/245,A61K39/29,A61K48/00,
                                                                                                                                                                                                                                       source
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/db_xref="taxon:32630"
7 c 3 g 3 t
                                                                                                                                                           /organism='Artificial Location/Qualifiers
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1. .14
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/db_xref="taxon:32630"
7 c 3 g 3 t
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                                                                                                                                                                                               Sequence'
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Query Match 100.0%; Score 6; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 1 ccgttc 6
| | | | | | | |
Db 4 CCGTTC 9
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Search completed: July 29, 2002, 23:55:06 Job time: 7022 sec